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ANTIRETROVIRAL THERAPY AND GUIDING THERAPEUTIC DECISIONS IN THE  
TREATMENT OF HIV/AIDS

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(54) Title: MEANS AND METHODS FOR MONITORING PROTEASE INHIBITOR ANTIRETROVIRAL THERAPY AND GUIDING THERAPEUTIC DECISIONS IN THE TREATMENT OF HIV/AIDS

(57) Abstract: This invention relates to antiviral drug susceptibility and resistance tests to be used in identifying effective drug regimens for the treatment of human immunodeficiency virus (HIV) infection and acquired immunodeficiency syndrome (AIDS), particularly treatment regimens including a protease inhibitor. The invention further relates to the means and methods of monitoring the clinical progression of HIV infection and its response to antiretroviral therapy using phenotypic or genotypic susceptibility assays.

MEANS AND METHODS FOR MONITORING PROTEASE  
INHIBITOR ANTIRETROVIRAL THERAPY AND GUIDING  
THERAPEUTIC DECISIONS IN THE TREATMENT OF HIV/AIDS

This application claims the benefit of U.S. Application No. 09/874,472 filed June 4, 2001, and PCT International Application No. PCT/US02/01682, filed January 18, 2002, the contents of which are hereby incorporated by reference into this application.

5 Throughout this application, various references are referred to within parenthesis. Disclosures of these publications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains.

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Technical Field

This invention relates to antiretroviral drug susceptibility and resistance tests to be used in identifying effective drug regimens for the treatment of human immunodeficiency virus (HIV) infection and acquired immunodeficiency syndrome (AIDS).  
15 The invention further relates to the means and methods of monitoring the clinical progression of HIV infection and its response to antiretroviral therapy using phenotypic or genotypic susceptibility assays. The invention also relates to novel vectors, host cells and compositions for carrying out phenotypic susceptibility tests. The invention further relates to the use of various genotypic methodologies to identify patients who do not respond to a particular antiretroviral drug regimen. This invention also relates to the screening of candidate antiretroviral drugs for their capacity to inhibit  
20 viral replication,  
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selected viral sequences and/or viral proteins. More particularly, this invention relates to the determination of protease inhibitor (PRI) susceptibility using phenotypic or genotypic susceptibility tests. This invention also relates to a means and method for accurately and reproducibly measuring viral replication fitness.

Background of the Invention

HIV infection is characterized by high rates of viral turnover throughout the disease process, eventually leading to CD4 depletion and disease progression. Wei X, Ghosh SK, Taylor ME, et al. (1995) *Nature* 343, 117-122 and Ho DD, Naumann AU, Perelson AS, et al. (1995) *Nature* 373, 123-126. The aim of antiretroviral therapy is to achieve substantial and prolonged suppression of viral replication. Achieving sustained viral control is likely to involve the use of sequential therapies, generally each therapy comprising combinations of three or more antiretroviral drugs. Choice of initial and subsequent therapy should, therefore, be made on a rational basis, with knowledge of resistance and cross-resistance patterns being vital to guiding those decisions. The primary rationale of combination therapy relates to synergistic or additive activity to achieve greater inhibition of viral replication. The tolerability of drug regimens will remain critical, however, as therapy will need to be maintained over many years.

In an untreated patient, some  $10^{10}$  new viral particles are produced per day. Coupled with the failure of HIV reverse transcriptase (RT) to correct transcription errors by exonucleolytic proofreading, this high level of viral

turnover results in  $10^4$  to  $10^5$  mutations per day at each position in the HIV genome. The result is the rapid establishment of extensive genotypic variation. While some template positions or base pair substitutions may be 5 more error prone (Mansky LM, Temin HM (1995) J Virol 69, 5087-5094) (Schinazi RF, Lloyd RM, Ramanathan CS, et al. (1994) Antimicrob Agents Chemother 38, 268-274), mathematical modeling suggests that, at every possible 10 single point, mutation may occur up to 10,000 times per day in infected individuals.

For antiretroviral drug resistance to occur, the target enzyme must be modified while preserving its function in the presence of the inhibitor. Point mutations leading to 15 an amino acid substitution may result in changes in shape, size or charge of the active site, substrate binding site or in positions surrounding the active site of the enzyme. Mutants resistant to antiretroviral agents have been detected at low levels before the initiation of therapy. 20 (Mohri H, Singh MK, Ching WTW, et al. (1993) Proc Natl Acad Sci USA 90, 25-29) (Nájera I, Richman DD, Olivares I, et al. (1994) AIDS Res Hum Retroviruses 10, 1479-1488) (Nájera I, Holguin A, Quiñones-Mateu E, et al. (1995) J Virol 69, 23-31). However, these mutant strains represent 25 only a small proportion of the total viral load and may have a replication or competitive disadvantage compared with wild-type virus. (Coffin JM (1995) Science 267, 483-489). The selective pressure of antiretroviral therapy provides these drug-resistant mutants with a 30 competitive advantage and thus they come to represent the dominant quasi species (Frost SDW, McLean AR (1994) AIDS 8, 323-332) (Kellam P, Boucher CAB, Tijagal JM GH (1994) J

Gen Virol 75, 341-351) ultimately leading to a rebound in viral load in the patient.

5 Early development of antiretroviral therapy focused on inhibitors of reverse transcriptase. Both nucleoside and non-nucleoside inhibitors of this enzyme showed significant antiviral activity (DeClerq, E. (1992) AIDS Res. Hum. Retrovir. 8:119-134). However, the clinical benefit of these drugs had been limited due to drug 10 resistance, limited potency, and host cellular factors (Richman, D.D. (1993) Ann. Rev. Pharm. Tox. 32:149-164). Thus inhibitors targeted against a second essential enzyme of HIV were urgently needed.

15 In 1988, the protease enzyme of HIV was crystallized and its three-dimensional structure was determined, (Navia MA, Fitzgerald PMD, McKeever BM, Leu CT, Heimbach JC, Herber WK, Sigal IS, Darke PL, Springer JP (1989) Nature 337:615-620 and Winters MA, Schapiro JM, Lawrence J, 20 Merigan TC (1997) In Abstracts of the International Workshop on HIV Drug Resistance, Treatment Strategies and Eradication, St. Petersburg, Fla.) allowing for the rapid development of protease inhibitors. Initially, it was hypothesized that HIV protease, unlike reverse 25 transcriptase, would be unable to accommodate mutations leading to drug resistance. This is not the case, and to date over 20 amino acid substitutions in the HIV protease have been observed during treatment with the currently available protease inhibitors. The genetic pattern of 30 mutations conferring resistance to these protease inhibitors is complex, and cross-resistance between structurally different compounds occurs.

PROTEASE INHIBITORS

HIV protease was classified as an aspartic proteinase on the basis of putative active-site homology (Toh H, Ono M, Saigo K, Miyata T (1985) *Nature* 315:691), its inhibition by peptastin (Richards AD, Roberts R, Dunn BM, Graves MC, Kay J (1989) *FEBS Lett* 247:113), and its crystal structure (Navia MA, Fitzgerald PMD, McKeever BM, Lau CT, Heimbach JC, Herber WK, Sigal IS, Darke PL, Springer JP (1989) *Nature* 337:615-620). The enzyme functions as a homodimer composed of two identical 99-amino acid chains (Debouck C, Navia MA, Fitzgerald PMD, McKeever BM, Leu CT, Heimbach JC, Herber WK, Sigal IS, Darke PL, Springer JP (1988) *Proc. Natl. Acad. Sci. USA* 84:8903-8906), with each chain containing the characteristic Asp-Thr-Gly active-site sequence at positions 25 to 27 (Toh H, Ono M, Saigo K, Miyata T (1985) *Nature* 315:691).

HIV protease processes gag (p55) and gag-pol (p160) polyprotein products into functional core proteins and viral enzymes (Kohl NE, Diehl RE, Rands E, Davis LJ, Hanobik MG, Wolanski B, Dixon RA (1991) *J. Virol.* 65:3007-3014 and Kramer RA, Schaber MD, Skalka AM, Ganguly K, Wong-Staal F, Reddy EP (1986) *Science* 231:1580-1584). During or immediately after budding, the polyproteins are cleaved by the enzyme at nine different cleavage sites to yield the structural proteins (p17, p24, p7, and p6) as well as the viral enzymes reverse transcriptase, integrase, and protease (Pettit SC, Michael SF, Swanstrom R (1993) *Drug Discov. Des.* 1:69-83).

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An asparagine replacement for aspartic acid at active-site residue 25 results in the production of noninfectious

viral particles with immature, defective cores (Huff JR (1991) AIDS J. Med. Chem. 34:2305-2314, Kaplan AH, Zack JA, Knigge M, Paul DA, Kempf DJ, Norbeck DW, Swanstrom R (1993) J. Virol. 67:4050-4055, Kohl NE, Emini EA, Schleif WA, Davis LJ, Heimbach JC, Dixon RA, Scolnik EM, Sigal IS (1988) Proc. Natl. Acad. Sci. USA 85:4686-4690, Peng C, Ho BK, Chang TW, Chang NT (1989) J. Virol. 63:2550-2556). Similarly, wild-type virus particles produced by infected cells treated with protease inhibitors contain unprocessed precursors and are noninfectious (Crawford S, Goff SP (1985) J. Virol. 53:899-907, Gottlinger HG, Sodroski JG, Haseltine WA (1989) Proc. Natl. Acad. Sci. USA 86:5781-5785, Katoh IY, Yoshinaka Y, Rein A, Shibuya M, Odaka T, Oroszlan S (1985) Virology 145:280-292, Kohl NE, Emini EA, Schleif WA, Davis LJ, Heimbach JC, Dixon RA, Scolnik EM, Sigal IS (1988) Proc. Natl. Acad. Sci. USA 85:4686-4690, Peng C, Ho BK, Chang TW, Chang NT (1989) J. Virol. 63:2550-2556, Stewart L, Schatz G, Wogt VM (1990) J. Virol. 64:5076-5092). Unlike reverse transcriptase inhibitors, protease inhibitors block the production of infectious virus from chronically infected cells (Lambert DM, Petteway, Jr. SR, McDanal CE, Hart TK, Leary JJ, Dreyer GB, Meek TD, Bugelski PJ, Bolognesi DP, Metcalf BW, Matthews TJ (1992) Antibicrob. Agents Chemother. 36:982-988). Although the viral protease is a symmetric dimer, it binds its natural substrates or inhibitors asymmetrically (Dreyer, GB, Boehm JC, Chenera B, DesJarlais RL, Hassell AM, Meek TD, Tomaszek TAJ, Lewis M (1993) Biochemistry 32:937-947, Miller MJ, Schneider J, Sathyanarayana BK, Toth MV, Marshall GR, Clawson L, Selk L, Kent SB, Wlodawer A (1989) Science 246:1149-1152). These findings together with the knowledge that amide

bonds of proline residues are not susceptible to cleavage by mammalian endopeptidases gave rise to the first class of HIV-1 protease inhibitors based on the transition state mimetic concept, with the phenylalanine-proline cleavage site being the critical nonscissile bond .(Roberts NA, Martin JA, Kinchington D, Broadhurst AV, Craig JC, Duncan IB, Galpin SA, Handa BK, Kay J, Krohn A, Lambert RW, Merett JH, Mills JS, Parkes KEB, Redshaw S, Ritchie AJ, Taylor DL, Thomas GJ, Machin PJ (1990) Science 10 248:358-361).

**Amino acids implicated in resistance to protease inhibitors.**

15 As new protease inhibitors are developed, the ability of certain amino acid substitutions to confer resistance to the inhibitor is usually determined by several methods, including selection of resistant strains in vitro, site-directed mutagenesis, and determination of amino acid changes that are selected during early phase clinical trials in infected patients. While some amino acid substitutions are specifically correlated with resistance to certain protease inhibitors (see below), there is considerable overlap between sets of mutations implicated 20 in resistance to all approved protease inhibitors. Many 25 investigators have attempted to classify these mutations as either being "primary" or "secondary", with varying definitions. For example, some investigators classify as primary mutations which are predicted, based on X-ray crystallographic data, to be in the enzyme active site 30 with the potential for direct contact with the inhibitor (e.g. D30N, G48V, I50V, V82A/F/S/T, I84V, N88S, L90M).

Secondary mutations are usually considered as being compensatory for defects in enzyme activity imposed by primary mutations, or as having enhancing effects on the magnitude of resistance imparted by the primary mutations (e.g. L10I/F/R/V, K20I/M/R/T, L24I, V32I, L33F/V, M36I/L/V, M46I/L/V, I47V, I54L/V, L63X, A71T/V, G73A/S/T, V77I, N88D). Lists of mutations and corresponding inhibitors are maintained by several organizations, for example: Schinazi et al., Mutations in retroviral genes associated with drug resistance, *Intl. Antiviral News* 1999, 7:46-69 and Shafer et al., Human Immunodeficiency Virus Reverse Transcriptase and Protease Sequence Database, *Nucleic Acids Research* 1999, 27(1), 348-352 (also accessible via the internet at <http://www.viral-resistance.com/> or <http://hivdb.stanford.edu/hiv/>)

Saquinavir

Saquinavir, developed by Hoffmann-La Roche, was the first protease inhibitor to undergo clinical evaluation, demonstrating that HIV-1 protease was a valid target for the treatment of HIV infection (Jacobsen H, Brun-Vezinet F, Duncan I, Hanggi M, Ott M, Vella S, Weber J, Mous J (1994) *J. Virol.* 68:2016-2020). Saquinavir is a highly active peptidomimetic protease inhibitor with a 90% inhibitory concentration (IC90) of 6 nM (*id*). In vitro, saquinavir can select for variants with one or both of two amino acid substitutions in the HIV-1 protease gene, a valine-for-glycine substitution at position 48 (G48V), a methionine-for-leucine substitution at residue 90 (L90M), and the double substitution G48V-L90M (Eberle J, Bechowsky B, Rose D, Hauser U, vonder Helm K, Guertler L, Nitschko H (1995) *AIDS Res. Hum. Retroviruses* 11:671-676, Jacobsen H, Yasargil K, Winslow DL, Craig JC, Kroehn A, Duncan IB, Mous J (1995) *Virology* 206:527-534, Turriziani O, Antonelli G, Jacobsen H, Mous J, Riva E, Pistello M, Dianzani F (1994) *Acta Virol.* 38:297-298). In most cases, G48V is the first mutation to appear, and continued selection results in highly resistant double-mutant variants. A substitution at either residue results in a 3- to 10-fold decreased susceptibility to the inhibitor, whereas the simultaneous occurrence of both substitutions causes a more severe loss of susceptibility of >100-fold (*id*).

In vivo, saquinavir therapy appears to select almost exclusively for mutations at codons 90 and 48 (*id*, Jacobsen H, Hangi M, Ott M, Duncan IB, Owen S, Andreoni M, Vella S, Mous J (1996) *J. Infect. Dis.* 173:1379-1387, Vella S, Galluzzo C, Giannini G, Pirillo MF, Duncan I,

Jacobsen H, Andreoni M, Sarmati L, Ercoli L (1996) Antiviral Res. 29:91-93). Saquinavir-resistant variants emerge in approximately 45% of patients after 1 year of monotherapy with 1,800 mg daily (Craig IC, Duncan IB, 5 Roberts NA, Whittaker L (1993) In Abstracts of the 9th International Conference on AIDS, Berlin, Germany, Duncan IB, Jacobsen H, Owen S, Roberts NA (1996) In Abstracts of the 3rd Conference of Retroviruses and Opportunistic Infections, Washington, D.D., id, Mous J, Brun-Vezinet F, 10 Duncan IB, Haenggi M, Jacobsen H, Vella S (1994) In Abstracts of the 10th International Conference on AIDS, Yokohama, Japan). The frequency of resistance is lower (22%) in patients receiving combination therapy with zidovudine, zalcitabine, and saquinavir (Collier AC, 15 Coombs R, Schoenfeld DA, Bassett RL, Joseph Timpone MS, Baruch A, Jones M, Facey K, Whitacre C, McAuliffe VJ, Friedman HM, Merigan TC, Reichmann RC, Hooper C, Corey L (1996) N. Engl. J. Med. 334:1011-1017). In contrast to in vitro-selected virus, where the G48V mutation is the first 20 step to resistance, the L90M exchange is the predominant mutation selected in vivo while the G48V (2%) or the double mutant (<2%) is rarely found (id). In another recent study of in vivo resistance during saquinavir monotherapy no patient was found to harbor a G48V mutant 25 virus (Ives KJ, Jacobsen H, Galpin SA, Garaev MM, Dorrell L, Mous J, Bragman K, Weber JN (1997 J. Antimicrob. Chemother. 39:771-779). Interestingly, Winters et al. (id) observed a higher frequency of the G48V mutation in patients receiving higher saquinavir doses as monotherapy. 30 All patients (six of six) who initially developed G48V also acquired a V82A mutation either during saquinavir treatment or after switching to either indinavir or

nelfinavir. An identical mutational pattern was found in another study during saquinavir monotherapy (Eastman PS, Duncan IB, Gee C, Race E (1997) In Abstracts of the International Workshop on HIV Drug Resistance, Treatment Strategies and Eradication, St. Petersburg, Fla.). Some residues represent sites of natural polymorphism of the HIV-1 protease (positions 10, 36, 63, and 71) and appear to be correlated to the L90M mutation (id). Another substitution, G73S, has been recently identified and may play a role in saquinavir resistance in vivo. Isolates from five patients with early saquinavir resistance and those from two patients with induced saquinavir resistance after a switch of therapy to indinavir carried the G73S and the L90M substitutions Dulioust A, Paulous S, Guillemot L, Boue F, Galanaud P, Clavel F (1997) In Abstracts of the International Workshop on HIV Drug Resistance, Treatment Strategies and Eradication, St. Petersburg, Fla.).

20 Ritonavir

Ritonavir, developed by Abbott Laboratories, was the second HIV protease inhibitor to be licensed in the United States. Ritonavir is a potent and selective inhibitor of HIV protease that is derived from a C2-symmetric, peptidomimetic inhibitor (Ho DD, Toyoshima T, Mo H, Kempf DJ, Norbeck D, Chen CM, Wideburg NE, Burt SK, Erickson JW, Singh MK (1994) J. Virol. 68:2016-2020). In vitro activity has been demonstrated against a variety of laboratory strains and clinical isolates of HIV-1 with IC90s of 70 to 200 nM (Kuroda MJ, El-Farrash MA, Clougherty S, Harada S (1995) Virology 210:212-216.

Resistant virus generated by serial in vitro passages is associated with specific mutations at positions 84, 82, 71, 63, and 46 (Markowitz M, Mo H, Kempf DJ, Norbeck DW, Bhat TN, Erickson JW, Ho DD (1995) J. Virol. 69:701-706).

5 The I84V substitution appeared to be the major determinant of resistance, resulting in a 10-fold reduction in sensitivity to ritonavir. Addition of the V82F mutation confers an even greater level of resistance, up to 20-fold. The substitutions M46I, L63P, and A71V, when

10 introduced into the protease coding region of wild-type NL4-3, did not result in significant changes in drug susceptibility. Based on replication kinetics experiments, these changes are likely to be compensatory for active-site mutations, restoring the impaired

15 replicative capacity of the combined V82F and I84V mutations.

Indinavir

Indinavir, developed by Merck & Co., is the third HIV protease inhibitor licensed in the United States. Indinavir is a potent and selective inhibitor of HIV-1 and 5 HIV-2 proteases with  $K_i$  values of 0.34 and 3.3 nM, respectively (Vacca Jp, Dorsey BD, Schleif WA, Levin RB, McDaniel SL, Darke PL, Zugay J, Quintero JC, Blahy OM, Roth E, Sardana VV, Schlabach AJ, Graham PI, Condra JH, Gotlib L, Holloway MK, Lin J, Chen L-w, Vastag K, Ostobich D, Anderson PS, Emini EA, Huff JR (1994) Proc. Natl. Acad. Sci. USA 91:4096-4100). The drug acts as peptidomimetic transition state analogue and belongs to the class of protease inhibitors known as HAPA (hydroxyaminopentane amide) compounds (ibid). Indinavir provides enhanced 10 aqueous solubility and oral bioavailability and in cell culture exhibits an IC<sub>95</sub> of 50 to 100 nM (Emini EA, Schleif WA, Deutsch P, Condra JH (1996) Antiviral 15 Chemother. 4:327-331.

20 Despite early reports of a lack of in vitro resistance by selection with indinavir (id), Tisdale et al. (Tisdale M, Myers RE, Maschera B, Parry NR, Oliver NM, Blair ED (1995) Antibicrob. Agents Chemother. 39:1704-1710) were able to obtain resistant variants during selection in MT-4 cells 25 with substitutions at residues 32, 46, 71, and 82. At least four mutations were required to produce a significant loss of susceptibility (6.1-fold compared with the wild type). The mutation at position 71, described as compensatory (Markowitz M, Mo H, Kempf DJ, Norbeck DW, Bhat TN, Erickson JW, Ho DD (1995) J. Virol. (id), 30 appeared to contribute phenotypic resistance and also to improve virus growth. Emini et al. (id) and Condra et al.

(Condra JH, Holder DJ, Schleif WA, Blahy OM, Danovich RM, Gabryelski LJ, Graham DJ, Laird D, Quintero JC, Rhodes A, Robbins HL, Roth E, Shivaprakash M, Yang T, Chodakewitz JA, Deutsch PJ, Leavitt RY, Massari Fe, Mellors JW, 5 Squires KE, Steigbigel RT, Teppler H, Emini EA (1995) Nature 374:569-571) found by constructing mutant HIV-1 clones that at least three mutations at residues 46, 63, and 82 were required for the phenotypic manifestation of resistance with a fourfold loss of susceptibility.

Nelfinavir

Nelfinavir, developed by Agouron Pharmaceuticals, is a selective, nonpeptidic HIV-1 protease inhibitor that was designed by protein structure-based techniques using iterative protein crystallographic analysis (Appelt KR, Bacquet J, Bartlett C, Booth CLJ, Freer ST, Fuhray MM, Gehring MR, Herrmann SM, Howland EF, Janson CA, Jones TR, Kan CC, Katharadekar V, Lewis KK, Marzoni GP, Mathews DA, Mohr C, Moomaw EW, Morse CA, Oatley SJ, Ogden RC, Reddy MR, Reich SH, Schoettlin WS, Smith WW, Varney MD, Villafranca JE, Ward RW, Webber S, Webber SE, Welsh KM, White J (1991) *J. Med. Chem.* 34:1925-1928). In vitro, nelfinavir was found to be a potent inhibitor of HIV-1 protease with a *Ki* of 2.0 nM (Kaldor SW, Kalish VJ, Davies JF, Shetty BV, Fritz JE, Appelt K, Burgess JA, Campanale KM, Chirgadze NY, Clawson DK, Dressman BA, Hatch SD, Khalil DA, Kosa MB, Lubbehusen PP, Muesing MA, Patrick AK, Reich SH, Su KS, Tatlock JH (1997) *J. Med. Chem.* 40:3979-3985). The drug demonstrated antiviral activity against several laboratory and clinical HIV-1 and HIV-2 strains with 50% effective concentrations ranging from 9 to 60 nM (Patrick AK, Boritzki TJ, Bloom LA (1997) *Antimicrob. Agents Chemother.* 41:2159-2164). Nelfinavir exhibits additive-to-synergistic effects when combined with other antiretroviral drugs (Partaledis JA, Yamaguchi AK, Tisdale M, Blair EE, Falcione C, Maschera B, Myers RE, Pazhanisamy S, Futer O, Bullinan AB, Stuver CM, Byrn RA, Livingston DJ (1995) *J. Virol.* 69:5228-5235). Preclinical data showed high levels of the drug in mesenteric lymph nodes and the spleen and good oral bioavailability (Shetty BV, Kosa MB, Khalil DA, Webber S (1996) *Antimicrob. Agents Chemother.* 40:110-114).

*In vitro*, following 22 serial passages of HIV-1<sub>NL4-3</sub> in the presence of nelfinavir, a variant (P22) with a sevenfold reduced susceptibility was isolated. After an additional six passages a variant (P28) with a 30-fold-decreased 5 susceptibility to nelfinavir was identified (Patick AK, Ho H, Markowitz M, Appelt K, Wu B, Musick L, Kaldor S, Reich S, Ho D, Webber S (1996) *Antimicrob. Agents Chemother.* 40:292-297). Sequence analysis of the protease gene from these variants identified in decreasing frequency the 10 substitutions D30N, A71V, and I84V for the P22 variant and mutations M46I, I84V/A, L63P, and A71V for the P28 variant. Antiviral susceptibility testing of recombinant mutant HIV-1<sub>NL4-3</sub> containing various mutations resulted in a 15 fivefold-increased 90% effective concentration for the I84V and D30N single mutants and the M46I/I84V double mutant, whereas no change in susceptibility was observed with M46I, L63P, or A71V alone (*ibid*).

Amprenavir

Amprenavir is a novel protease inhibitor developed by Vertex Laboratories and designed from knowledge of the HIV-1 protease crystal structure (Kim EE, Baker CT, Dyer MD, Murcko MA, Rao BG, Tung RD, Navia MA (1995) J. Am. Chem. Soc. 117:1181-1182). The drug belongs to the class of sulfonamide protease inhibitors and has been shown to be a potent inhibitor of HIV-1 and HIV-2, with IC50s of 80 and 340 nM, respectively. The mean IC50 for amprenavir against clinical viral isolates was 12 nM (St. Clair MH, Millard J, Rooney J, Tisdale M, Parry N, Sadler BM, Blum MR, Painter G (1996) Antiviral Res. 29:53-56). HIV-1 variants 100-fold resistant to amprenavir have been selected by in vitro passage experiments (id). DNA sequence analysis of the protease of these variants revealed a sequential accumulation of point mutations resulting in amino acid substitutions L10F, M46I, I47V, and I50V. The key resistance mutation in the HIV-1 protease substrate binding site is I50V. As a single mutation it confers a two- to threefold decrease in susceptibility (ibid). The other substitutions did not result in reduced susceptibility when introduced as single mutations into an HIV-1 infectious clone (HXB2). However, a triple protease mutant clone containing the mutations M46I, I47V, and I50V was 20-fold less susceptible to amprenavir than wild-type virus. The I50V mutation has not been frequently reported in resistance studies with other HIV protease inhibitors. Kinetic characterization of these substitutions demonstrated an 80-fold reduction in the inhibition constant ( $K_i$ ) for the I50V single-mutant protease and a 270-fold-reduced  $K_i$  for the triple mutant M46I/I47V/I50V, compared to the wild-type enzyme.

(Pazhanisamy S, St6uvr CM, Cullinan AB, Margolin N, Rao BG (1996) J. Biol. Chem. 271:17979-17985). The single mutants L10F, M46I, and I47V did not display reduced affinity for amprenavir. The catalytic efficiency ( $k_{cat}/K_m$ ) of the I50V mutant was decreased up to 25-fold, while the triple mutant M46I/I47V/I50V had a 2-fold-higher processing efficiency than the I50V single mutant, confirming the compensatory role of the M46I-and-I47V mutation. The reduced catalytic efficiency ( $k_{cat}/K_m$ ) for these mutants in processing peptides appeared to be due to both increased  $K_m$  and decreased  $k_{cat}$  values.

#### VIRAL FITNESS

The relative ability of a given virus or virus mutant to replicate is termed viral fitness. Fitness is dependent on both viral and host factors, including the genetic composition of the virus, the host immune response, and selective pressures such as the presence of anti-viral compounds. Many drug-resistant variants of HIV-1 are less fit than the wild-type, i.e. they grow more slowly in the absence of drug selection. However, since the replication of the wild-type virus is inhibited in the presence of drug, the resistant mutant can outgrow it. The reduction in fitness may be a result of several factors including: decreased ability of the mutated enzyme (i.e. PR or RT) to recognize its natural substrates, decreased stability of the mutant protein, or decreased kinetics of enzymatic catalysis. See Back et al., EMBO J. 15: 4040-4049, 1996; Goudsmit et al., J. Virol. 70: 5662-5664, 1996; Maschera et al., J. Biol. Chem. 271: 33231-33235, 1996; Croteau et al., J. Virol. 71: 1089-1096, 1997; Zennou et al., J. Virol. 72: 300-3306, 1998; Harrigan et al., J. Virol. 72:

3773-3778, 1998; Kosalaraksa et al., *J. Virol.* 73: 5356-5363, 1999; Gerondelis et al., *J. Virol.* 73: 5803-5813, 1999. Drug resistant viruses that are less fit than wild type may be less virulent i.e. they may cause 5 damage to the host immune system more slowly than a wild type virus. Immunological decline may be delayed after the emergence of drug resistant mutants, compared to the rate of immunological decline in an untreated patient. The defect causing reductions in fitness may be partially or 10 completely compensated for by the selection of viruses with additional amino acid substitutions in the same protein that bears the drug resistance mutations (for example, see Martinez-Picado et al., *J. Virol.* 73:3744-3752, 1999), or in other proteins which interact 15 with the mutated enzyme. Thus, amino acids surrounding the protease cleavage site in the gag protein may be altered so that the site is better recognized by a drug-resistant protease enzyme (Doyon et al., *J. Virol.* 70: 3763-3769, 1996; Zhang et al., *J. Virol.* 71: 6662-6670, 1997; Mammano 20 et al., *J. Virol.* 72: 7632-7637, 1998).

#### INTEGRASE

Integration of viral DNA into the host chromosome is a necessary process in the HIV replication cycle (Brown, 25 P.O., 1997, in *Retroviruses*; Coffin, J.M., Hughes, S.H. & Varmus, H.E., eds., Cold Spring Harbor Lab. Press, Plainview, NY, 161-203). The key steps of DNA integration are carried out by the viral integrase protein, which, along with protease and reverse transcriptase, is one of 30 three enzymes encoded by HIV. Combination antiviral therapy with protease and reverse transcriptase inhibitors has demonstrated the potential therapeutic efficacy of

antiviral therapy for treatment for AIDS (Vandamme, A.M., Van Vaerenbergh, K. & De Clerq, E., 1998, *Antiviral Chem. Chemother.* 9, 187-203). However, the ability of HIV to rapidly evolve drug resistance, together with toxicity problems, requires the development of additional classes of antiviral drugs. Integrase is an attractive target for antivirals because it is essential for HIV replication and, unlike protease and reverse transcriptase, there are no known counterparts in the host cell. Furthermore, 5 integrase uses a single active site to accommodate two different configurations of DNA substrates, which may constrain the ability of HIV to develop drug resistance to integrase inhibitors. However, unlike protease and reverse transcriptase, for which several classes of 10 inhibitors have been developed and cocrystal structures have been determined, progress with the development of integrase inhibitors has been slow. A major obstacle has 15 been the absence of good lead compounds that can serve as the starting point for structure-based inhibitor development. Although numerous compounds have been 20 reported to inhibit integrase activity in vitro, most of these compounds exhibit little specificity for integrase and are not useful as lead compounds (Pommier, Y., Pilon, A.A., Bajaj K, K., Mazumder, A. & Neamati, N., 1997, 25 *Antiviral Chem. Chemother* 8).

HIV-1 integrase is a 32-kDa enzyme that carries out DNA integration in a two-step reaction (Brown, P.O., *ibid.*). In the first step, called 3' processing, two nucleotides 30 are removed from each 3' end of the viral DNA made by reverse transcription. In the next step, called DNA strand transfer, a pair of transesterification reactions

integrates the ends of the viral DNA into the host genome. Integrase is comprised of three structurally and functionally distinct domains, and all three domains are required for each step of the integration reaction

5 (Engelman, A., Bushman, F.D. & Craigie, R., 1993, *EMBO J.* 12, 3269-3275). The isolated domains form homodimers in solution, and the three-dimensional structures of all three separate dimers have been determined (Dyda, F., Hickman, A.B., Jenkins, T.M., Engelman, A., Craigie, R. &

10 Davies, D.R., 1994, *Science* 226, 1981-1986; Goldgur, Y., Dyda, F., Hickman, A.B., Jenkins, T.M., Craigie, R. & Davies, D.R., 1998, *Proc. Natl. Acad. Sci., USA* 95, 9150-9154; Maignan, S., Guilloteau, J.P., Zhou-Liu, Q., Clement-Mella, C. & Mikol, V., 1998, *J Mol. Biol.* 282, 259-368;

15 Lodi, P.J., Ernst, J.A., Kuszewski, J., Hickman, A.B., Engelman, A., Craigie, R., Clore, G.M. & Gronenborn, A.M. 1995 *Biochemistry* 34, 9826-9833; Eijkelenboom, A.P., Lutzke, R.A., Boelens, R., Plasterk, R.H., Kaptein, R. & Hard, K. 1995 *Nat. Struct. Biol.* 2, 807-810; Cai, M.L.,

20 Zheng, R., Caffrey, M., Craigie, R., Clore, G.M. & Gronenborn, A.M., 1997 *Nat. Struct. Biol.* 4, 839-840). Although little is known concerning the organization of these domains in the active complex with DNA substrates, integrase is likely to function as at least a tetramer

25 (Dyda, F., Hickman, A.B., Jenkins, T.M., Engelman, A., Craigie, R. & Davies, D.R., 1994, *Science* 226, 1981-1986). Extensive mutagenesis studies mapped the catalytic site to the core domain (residues 50-212), which contains the catalytic residues D64, D116, and E152 (Engelman, A. &

30 Craigie R., 1992, *J. Virol.* 66, 6361-6369; Kulkosky, J., Jones, K.S., Katz, R.A., Mack, J.P. & Skalka, A.M., 1992, *Mol. Cell Biol* 12, 2331-2338). The structure of this

domain of HIV-1 integrase has been determined in several crystal forms (Dyda, F., Hickman, A.B. Jenkins, T.M., Engelman, A., Craigie, R. & Davies, D.R., 1994, *Science* 262, 1981-1986; Goldgur, Y. Dyda, Hickman, A.B., Jenkins, T.M., Craigie, R. & Davies, D.R., 1998, *Proc. Natl. Acad. Sci., USA* 95, 9150-9154; Maignan, S., Guilloteau, J.P., Zhou-Liu, Q., Clement-Mella, C. & Mikol, V., 1998, *J Mol. Biol.* 282, 259-368).

10 Hazuda et al. (Science 287: 646-650, 2000) have described compounds (termed L-731, 988 and L-708,906) which specifically inhibit the strand-transfer activity of HIV-1 integrase and HIV-1 replication in vitro. Viruses grown in the presence of these inhibitors display reduced inhibitor susceptibility and bear mutations in the integrase coding region at amino acid positions 66 (T66I), 153 (S153Y), and 154 (M154I). Site-directed mutants of a laboratory strain of HIV-1 (HXB2) with these amino acid changes confirmed their direct role in conferring reduced integrase inhibitor susceptibility. In addition some of these mutants displayed delayed growth kinetics, suggesting that viral fitness was impaired.

25 It is an object of this invention to provide a drug susceptibility and resistance test capable of showing whether a viral population in a patient is either more or less susceptible to a given prescribed drug. Another object of this invention is to provide a test that will enable the physician to substitute one or more drugs in a therapeutic regimen for viruses that show altered susceptibility to a given drug or drugs after a course of therapy. Yet another object of this invention is to

provide a test that will enable selection of an effective drug regimen for the treatment of HIV infections and/or AIDS. Yet another object of this invention is to provide the means for identifying alterations in the drug 5 susceptibility profile of a patient's virus, in particular identifying changes in susceptibility to protease inhibitors. Still another object of this invention is to provide a test and methods for evaluating the biological effectiveness of candidate drug compounds which act on 10 specific viruses, viral genes and/or viral proteins particularly with respect to alterations in viral drug susceptibility associated with protease inhibitors. It is also an object of this invention to provide the means and 15 compositions for evaluating HIV antiretroviral drug resistance and susceptibility.

It is an object of this invention to provide a method for measuring replication fitness which can be adapted to viruses, including, but not limited to human 20 immunodeficiency virus (HIV), hepadnaviruses (human hepatitis B virus), flaviviruses (human hepatitis C virus) and herpesviruses (human cytomegalovirus). This and other objects of this invention will be apparent from the specification as a whole.

Summary of the Invention

The present invention relates to methods of monitoring, via phenotypic and genotypic methods the clinical progression of human immunodeficiency virus infection and its response to antiviral therapy. The invention is also based, in part, on the discovery that genetic changes in HIV protease (PR) which confer changes in susceptibility to antiretroviral therapy may be rapidly determined directly from patient plasma HIV RNA using phenotypic or genotypic methods. The methods utilize nucleic acid amplification based assays, such as polymerase chain reaction (PCR). Herein—after, such nucleic acid amplification based assays will be referred to as PCR based assays. This invention is based in part on the discovery of mutations at codons 10, 20, 36, 46, 63, 77 and 88 of HIV protease in PRI treated patients in which the presence of certain combinations of these mutations correlate with changes in certain PRI susceptibilities. This invention is also based on the discovery that susceptibility to HIV protease antivirals may not be altered even if primary mutations are present. Additional mutations at secondary positions in HIV protease are required for a reduction in virus susceptibility. This invention established for the first time that a mutation at position 82 of protease (V82A, F, S, or T) in the absence of another primary mutation was not correlated with a reduction in drug susceptibility. Decreased susceptibility to protease inhibitors, such as indinavir and saquinavir, in viruses containing V82A, F, S or T was observed in viruses with additional mutations at secondary positions, such as, 24, 71, 54, 46, 10 and/or 63 as described herein. Decreased susceptibility to protease

inhibitors, such as indinavir and saquinavir, in viruses containing V82A, F, S or T was also observed in viruses with at least 3 or more additional mutations at secondary positions. This inventions also established for the first 5 time that a mutation at position 90 of protease (L90M) in the absence of another primary mutation was not correlated with a reduction in drug susceptibility. Decreased susceptibility to protease inhibitors, such as indinavir and saquinavir, in viruses containing L90M was observed in 10 viruses with additional mutations at secondary positions, such as, 73, 71, 77, and/or 10 as described herein. Decreased susceptibility to protease inhibitors, such as indinavir and saquinavir, in viruses containing L90M was also observed in viruses with at least 3 or more 15 additional mutations at secondary positions. The mutations were found in plasma HIV nucleic acid after a period of time following the initiation of therapy. The development of these mutations, or combinations of these mutations, in HIV PR was found to be an indicator of the development of 20 alterations in phenotypic susceptibility/resistance, which can be associated with virologic failure and subsequent immunological response.

In one embodiment of the invention, a method of assessing 25 the effectiveness of protease antiretroviral therapy of an HIV-infected patient is provided comprising: (a) collecting a plasma sample from the HIV-infected patient; (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at primary and 30 secondary positions; and (c) determining changes in susceptibility to a protease inhibitor.

In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be used to detect a substitution at codon 88 from asparagine to a serine residue either alone or in combination with 5 one or more mutations at other codons selected from the group consisting of 10, 20, 36, 46, 63 and/or 77 or a combination thereof of HIV PR. A mutation at codon 88 from an asparagine residue to a serine residue (N88S) alone correlates with an increase in susceptibility to 10 amprenavir and a mutation at codon 88 from an asparagine residue to a serine residue in combination with mutations at codons 63 and/or 77 or a combination thereof correlates with an increase in susceptibility to amprenavir and a decrease in nelfinavir and indinavir susceptibility.

15 In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be used to detect mutations at codons 10, 20, 36, 46, 63, 77, and 88 of HIV PR which correlate with changes in 20 susceptibility to antiretroviral therapy and immunologic response. Once mutations at these loci have been detected in a patient undergoing PRI antiretroviral therapy, an alteration in the therapeutic regimen should be considered. The timing at which a modification of the 25 therapeutic regimen should be made, following the assessment of antiretroviral therapy using PCR based assays, may depend on several factors including the patient's viral load, CD4 count, and prior treatment history.

30 In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be

used to detect a substitution at codon 82 from valine to an alanine (V82A), phenylalanine (V82F), serine (V82S), or threonine (V82T) residue either alone or in combination with one or more mutations at other codons, referred to 5 herein as secondary mutations, selected from the group consisting of 20, 24, 36, 71, 54, 46, 63 and/or 10 or a combination thereof of HIV PR. A mutation at codon 82 from a valine residue to a alanine, phenylalanine, serine or threonine alone correlates with susceptibility to 10 certain protease inhibitors including indinavir and saquinavir. A mutation at codon 82 from a valine residue to a alanine, phenylalanine, serine or threonine in combination with secondary mutations at codons 24 and/or 71 or 20 and/or 36 correlates with a reduction in 15 susceptibility to indinavir and saquinavir, respectively. A mutation at codon 82 from a valine residue to a alanine, phenylalanine, serine or threonine in combination with at least 3 secondary mutations correlates with a reduction in susceptibility to indinavir and saquinavir.

20 In a further embodiment of the invention, PCR based assays, including phenotypic and genotypic assays, may be used to detect a substitution at codon 90 from leucine to a methionine (L90M) residue either alone or in combination 25 with one or more mutations at other codons, referred to herein as secondary mutations, selected from the group consisting of 73, 71, 46 and/or 10 or a combination thereof of HIV PR. A mutation at codon 90 from a leucine residue to a methionine alone correlates with 30 susceptibility to certain protease inhibitors including indinavir and saquinavir. A mutation at codon 90 from a leucine residue to a methionine in combination with

secondary mutations at codons 73 and/or 71 or 73, 71 and/or 77 correlates with a reduction in susceptibility to indinavir and saquinavir, respectively. A mutation at codon 90 from a leucine residue to a methionine in combination with at least 3 secondary mutations correlates with a reduction in susceptibility to indinavir and saquinavir.

In another aspect of the invention there is provided a method for assessing the effectiveness of a protease inhibitor antiretroviral drug comprising: (a) introducing 10 a resistance test vector comprising a patient-derived segment and an indicator gene into a host cell; (b) culturing the host cell from step (a); (c) measuring expression of the indicator gene in a target host cell 15 wherein expression of the indicator gene is dependent upon the patient derived segment; and (d) comparing the expression of the indicator gene from step (c) with the expression of the indicator gene measured when steps (a) - (c) are carried out in the absence of the PRI anti-HIV 20 drug, wherein a test concentration of the PRI, anti-HIV drug is presented at steps (a) - (c); at steps (b) - (c); or at step (c).

This invention also provides a method for assessing the 25 effectiveness of protease inhibitor antiretroviral therapy in a patient comprising: (a) developing a standard curve of drug susceptibility for an PRI anti-HIV drug; (b) determining PRI anti-HIV drug susceptibility in the patient using the susceptibility test described above; and (c) comparing the PRI anti-HIV drug susceptibility in step 30 (b) with the standard curve determined in step (a), wherein a decrease in PRI anti-HIV susceptibility

indicates development of anti-HIV drug resistance in the patient's virus and an increase in PRI anti-HIV susceptibility indicates drug hypersensitivity in the patient's virus.

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This invention also provides a method for evaluating the biological effectiveness of a candidate PRI HIV antiretroviral drug compound comprising: (a) introducing a resistance test vector comprising a patient-derived segment and an indicator gene into a host cell; (b) culturing the host cell from step (a); (c) measuring expression of the indicator gene in a target host cell wherein expression of the indicator gene is dependent upon the patient derived segment; and (d) comparing the expression of the indicator gene from step (c) with the expression of the indicator gene measured when steps (a) - (c) are carried out in the absence of the candidate PRI anti-viral drug compound, wherein a test concentration of the candidate PRI anti-viral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

20

The expression of the indicator gene in the resistance test vector in the target cell is ultimately dependent upon the action of the HIV enzymes (PR and RT) encoded by the patient-derived segment DNA sequences. The indicator gene may be functional or non-functional.

25 30

In another aspect this invention is directed to antiretroviral drug susceptibility and resistance tests for HIV/AIDS. Particular resistance test vectors of the invention for use in the HIV/AIDS antiretroviral drug susceptibility and resistance test are identified.

Yet another aspect of this invention provides for the identification and assessment of the biological effectiveness of potential therapeutic antiretroviral 5 compounds for the treatment of HIV and/or AIDS. In another aspect, the invention is directed to a novel resistance test vector comprising a patient-derived segment further comprising one or more mutations on the PR gene and an indicator gene.

10

Still another aspect of this invention provides for the identification and assessment of the fitness of a virus infecting a patient. In another aspect, the invention is directed to a novel resistance test vector comprising a 15 patient-derived segment further comprising one or more mutations on the PR gene and an indicator gene, enabling the measurement of viral fitness.

Brief Description of the Drawings

## Fig. 1

Resistance Test Vector. A diagrammatic representation of  
5 the resistance test vector comprising a patient derived  
segment and an indicator gene.

## Fig. 2

Two Cell Assay. Schematic Representation of the Assay. A  
10 resistance test vector is generated by cloning the  
patient-derived segment into an indicator gene viral  
vector. The resistance test vector is then co-transfected  
with an expression vector that produces amphotropic murine  
leukemia virus (MLV) envelope protein or other viral or  
15 cellular proteins which enable infection. Pseudotyped  
viral particles are produced containing the protease (PR)  
and the reverse transcriptase (RT) gene products encoded  
by the patient-derived DNA sequences. The particles are  
then harvested and used to infect fresh cells. Using  
20 defective PR and RT sequences it was shown that luciferase  
activity is dependent on functional PR and RT. PR  
inhibitors are added to the cells following transfection  
and are thus present during particle maturation. RT  
inhibitors, on the other hand, are added to the cells at  
25 the time of or prior to viral particle infection. The  
assay is performed in the absence of drug and in the  
presence of drug over a wide range of concentrations.  
Luciferase activity is determined and the percentage (%)  
inhibition is calculated at the different drug  
30 concentrations tested.

## Fig. 3

Examples of phenotypic drug susceptibility profiles. Data are analyzed by plotting the percent inhibition of luciferase activity vs.  $\log_{10}$  concentration. This plot is 5 used to calculate the drug concentration that is required to inhibit virus replication by 50% (IC50) or by 95% (IC95). Shifts in the inhibition curves towards higher drug concentrations are interpreted as evidence of drug 10 resistance. Three typical curves for a nucleoside reverse transcriptase inhibitor (AZT), a non-nucleoside reverse transcriptase inhibitor (efavirenz), and a protease inhibitor (indinavir) are shown. A reduction in drug 15 susceptibility (resistance) is reflected in a shift in the drug susceptibility curve toward higher drug concentrations (to the right) as compared to a baseline (pre-treatment) sample or a drug susceptible virus reference control, such as pNL4-3 or HXB-2, when a baseline sample is not available.

## 20 Fig. 4

Phenotypic PRI susceptibility profile: patient 0732. A PCR-based phenotypic susceptibility assay was carried out giving the phenotypic drug susceptibility profile showing decreased susceptibility to nelfinavir and indinavir, and 25 increased susceptibility to amprenavir.

## Fig. 5

Phenotypic PRI susceptibility profile of a protease mutant generated by site-specific oligonucleotide-directed 30 mutagenesis. A PCR-based phenotypic susceptibility assay was carried out giving the phenotypic drug susceptibility profile of a virus having substitutions at codons 63, 77

and 88 (L63P, V77I and N88S). The profile demonstrates resistance to both nelfinavir and indinavir, and increased susceptibility to amprenavir.

5 Figure 6. Distribution of saquinavir hyper-susceptibility by amino acid change at position 82.

Figure 7. Relative luciferase activity of integrase inhibitor-resistant site-directed mutants.

10

Fig. A

Two Cell Fitness Assay. Schematic Representation of the Fitness Assay. A fitness test vector is generated by cloning the patient-derived segment into an indicator gene viral vector. The fitness test vector is then co-transfected with an expression vector that produces amphotropic murine leukemia virus (MLV) envelope protein or other viral or cellular proteins which enable infection. Pseudotyped viral particles are produced containing the protease (PR) and the reverse transcriptase (RT) gene products encoded by the patient-derived DNA sequences. The particles are then harvested and used to infect fresh cells. Using defective PR and RT sequences it was shown that luciferase activity is dependent on functional PR and RT. The fitness assay is typically performed in the absence of drug. If desired, the assay can also be performed at defined drug concentrations. Luciferase activity produced by patient derived viruses is compared to the luciferase activity produced by well-characterized reference viruses. Replication fitness is expressed as a percent of the reference.

**Figure B.**

Determining the replication fitness of patient viruses. Virus stocks produced from fitness test vectors derived from patient samples were used to infect cells. 5 Luciferase activity was measured at various times after infection. Patient derived viruses may produce more, approximately the same, or less luciferase activity than the reference virus (Ref) and are said to have greater, equivalent, or reduced replication fitness, 10 respectively. The drug susceptibility profiles of three representative patient derived viruses are shown (P1, P2, P3).

**Figure C.**

15 Identifying alterations in protease or reverse transcriptase function associated with differences in replication fitness of patient viruses. Replication fitness is expressed as a percent of the reference virus (top). Fitness measurements are compared to protease processing of the p55 gag polyprotein (middle) and reverse transcriptase activity (bottom). Protease processing is measured by Western blot analysis using an antibody that reacts with the mature capsid protein (p24). The detection of unprocessed p55 or incompletely processed p41 polyproteins are indicators of reduced cleavage. Reverse transcriptase activity is measured using a quantitative RT-PCR assay and is expressed as a percent of the 20 reference virus.

**30 Figure D.**

Correlating reduced replication fitness with reduced reverse transcriptase activity. Viruses containing

various amino acid substitutions at position 190 (A, S, C, Q, E, T, V) of reverse transcriptase were constructed using site directed mutagenesis. The reference virus contains G at this position. Replication fitness and

5

reverse transcriptase activities were compared.

Figure E.

Correlating reduced replication fitness with reduced protease processing of p55 gag. Viruses containing various amino acid substitutions in protease (D30N, L90M, etc) were constructed using site directed mutagenesis. Replication fitness and p55 gag processing were compared.

15 Figure F.

Correlating reduced replication fitness with reduced drug susceptibility. A large collection (n=134) of patient samples were evaluated for phenotypic drug susceptibility and replication fitness. Replication fitness and drug susceptibility were compared.

Figure G.

Relationship between protease inhibitor susceptibility and replication fitness. Patient samples were sorted based on 25 their replication fitness (<25% of reference, 26-75% of reference, and >75% of reference). Mean values for protease inhibitor susceptibility were determined for each fitness group and plotted for each drug and all drugs combined.

30

Figure H.

Relationship between reverse transcriptase inhibitor

susceptibility and replication fitness. Patient samples were sorted based on their replication fitness (<25% of reference, 26-75% of reference, and >75% of reference). Mean values for reverse transcriptase susceptibility were 5 determined for each fitness group and plotted for each drug and all drugs combined.

Figure I.

Reduced replication fitness is associated with high 10 numbers of protease mutations, and the L90M mutation. Patient viruses were sorted based on the number of protease mutations. Viruses with large numbers of protease mutations or the L90M protease mutation generally exhibit reduced replication fitness.

15

Figure J.

Low replication capacity is associated with specific protease mutations. Patient viruses were sorted based on replication capacity. Specific protease mutations either 20 alone (D30N) or in combination (L90M plus others) were observed with high frequency in viruses with reduced replication fitness.

Figure K.

25 Relationship between nelfinavir susceptibility, protease processing and replication fitness. Patient viruses were sorted based on nelfinavir susceptibility (<10 or >10 of reference). Protease processing and replication fitness were plotted for all patient viruses. Viruses with 30 reduced nelfinavir susceptibility generally exhibited reduced protease processing and reduced replication fitness.

Figure L. Protease mutations associated with reduced protease processing. Patient viruses were sorted based on protease processing. Specific protease mutations were observed at high frequency in viruses with reduced protease processing.

Figure M.  
10 Representative patient sample exhibiting reversion to drug susceptibility during a period of drug treatment interruption. Virus samples were collected weekly during a period of treatment interruption and evaluated for phenotypic drug susceptibility. Values shown represent fold change in susceptibility compared to the reference 15 virus.

Figure N.  
20 Representative patient sample exhibiting increased replication fitness during a period of drug treatment interruption. Virus samples were collected weekly during a period of treatment interruption and evaluated for phenotypic drug susceptibility. Fitness values shown represent percent of the reference virus. The increase in fitness between week 9 and week 10 corresponds to improved 25 protease processing (bottom) and reversion of the drug resistant phenotype to a drug sensitive phenotype (Figure M).

Figure O.  
30 Increased replication fitness during treatment interruption. Replication fitness was measured at the time of treatment interruption and various times during

the period of treatment interruption. Generally, replication fitness was significantly higher in samples that corresponded to timepoints after the virus had reverted from a drug resistant phenotype to a drug 5 sensitive phenotype.

Detailed Description of the Invention

10 The present invention relates to methods of monitoring the clinical progression of HIV infection in patients receiving antiretroviral therapy, particularly protease inhibitor antiretroviral therapy.

15 In one embodiment, the present invention provides for a method of evaluating the effectiveness of antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises 20 nucleic acid encoding HIV PR having a mutation at one or more positions in the PR. The mutation(s) correlate positively with alterations in phenotypic susceptibility.

25 In a specific embodiment, the invention provides for a method of evaluating the effectiveness of PRI antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises nucleic acid encoding HIV PR having a 30 mutation at codon 88 from an asparagine residue to a serine residue (N88S). This invention established, using a phenotypic susceptibility assay, that a mutation at

codon 88 to a serine residue of HIV protease is correlated with an increase in amprenavir susceptibility.

In a specific embodiment, the invention provides for a 5 method of evaluating the effectiveness of PRI antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises nucleic acid encoding HIV PR having a 10 mutation at codon 88 from an asparagine residue to a serine residue (N88S) either alone or in combination with mutations at codons 63 and/or 77 or a combination thereof. This invention established, using a phenotypic 15 susceptibility assay, that a mutation at codon 88 to a serine residue of HIV protease is correlated with an increase in amprenavir susceptibility and a mutation at codon 88 to a serine residue in combination with mutations at codons 63 and/or 77 or a combination thereof of HIV 20 protease are correlated with an increase in amprenavir susceptibility and a decrease in nelfinavir and indinavir susceptibility.

In a specific embodiment, the invention provides for a 25 method of evaluating the effectiveness of PRI antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises nucleic acid encoding HIV PR having a mutation at codon 88 from an asparagine residue to a 30 serine residue (N88S) either alone or in combination with mutations at codons 46, 63 and/or 77 or a combination thereof. This invention established, using a phenotypic

susceptibility assay, that a mutation at codon 88 to a serine residue of HIV protease is correlated with an increase in amprenavir susceptibility and a mutation at codon 88 to a serine residue in combination with mutations at codons 46, 63 and/or 77 or a combination thereof of HIV protease are correlated with an increase in amprenavir susceptibility and a decrease in nelfinavir and indinavir susceptibility.

10 In a specific embodiment, the invention provides for a method of evaluating the effectiveness of PRI antiretroviral therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; and (ii) determining whether the biological sample comprises nucleic acid encoding HIV PR having a mutation at codon 88 from an asparagine residue to a serine residue (N88S) either alone or in combination with mutations at codons 10, 20, 36, 46, 63 and/or 77 or a combination thereof. This invention established, using a phenotypic susceptibility assay, that a mutation at codon 88 to a serine residue of HIV protease is correlated with an increase in amprenavir susceptibility and a mutation at codon 88 to a serine residue in combination with mutations at codons 10, 20, 36, 46, 63 and/or 77 or a combination thereof of HIV protease are correlated with an increase in amprenavir susceptibility and a decrease in nelfinavir and indinavir susceptibility.

Under the foregoing circumstances, the phenotypic susceptibility profile and genotypic profile of the HIV virus infecting the patient has been altered reflecting a change in response to the antiretroviral agent. In the

case of PRI antiretroviral therapy, the HIV virus infecting the patient may be resistant to one or more PRIs but hypersensitive to another of the PRIs as described herein. It therefore may be desirable after detecting the 5 mutation(s), to either increase the dosage of the antiretroviral agent, change to another antiretroviral agent, or add one or more additional antiretroviral agents to the patient's therapeutic regimen. For example, if the patient was being treated with nelfinavir when the N88S 10 mutation arose, the patient's therapeutic regimen may desirably be altered by either (i) changing to a different PRI antiretroviral agent, such as saquinavir, ritonavir or amprenavir and stopping nelfinavir treatment; or (ii) increasing the dosage of nelfinavir; or (iii) adding 15 another antiretroviral agent to the patient's therapeutic regimen. The effectiveness of the modification in therapy may be further evaluated by monitoring viral burden such as by HIV RNA copy number. A decrease in HIV RNA copy number correlates positively with the effectiveness of a 20 treatment regimen.

The phrase "correlates positively," as used herein, indicates that a particular result renders a particular conclusion more likely than other conclusions.

25 When reference is made to a particular codon number, it is understood that the codon number refers to the position of the amino acid that the codon codes for. Therefore a codon referencing a particular number is equivalent to a 30 "position" referencing a particular number, such as for example, "codon 88" or "position 88".

Another preferred, non-limiting, specific embodiment of the invention is as follows: A method of evaluating the effectiveness of PRI therapy of a patient comprising (i) collecting a biological sample from an HIV-infected 5 patient; (ii) purifying and converting the viral RNA to cDNA and amplifying HIV sequences using HIV primers that result in a PCR product that comprises the PR gene; (iii) performing PCR using primers that result in PCR products comprising wild type or serine at codon 88; and (iv) 10 determining, via the products of PCR, the presence or absence of a serine residue at codon 88.

Another preferred, non-limiting, specific embodiment of the invention is as follows: A method of evaluating the 15 effectiveness of PRI therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; (ii) purifying and converting the viral RNA to cDNA and amplifying HIV sequences using HIV primers that result in a PCR product that comprises the PR gene; (iii) 20 performing PCR using primers that result in PCR products comprising wild type or serine at codon 88 and mutations at codons 63 and/or 77; and (iv) determining, via the products of PCR, the presence or absence of a serine residue at codon 88 and the presence or absence of 25 mutations at codons 63 and/or 77.

Another preferred, non-limiting, specific embodiment of the invention is as follows: A method of evaluating the effectiveness of PRI therapy of a patient comprising (i) 30 collecting a biological sample from an HIV-infected patient; (ii) purifying and converting the viral RNA to cDNA and amplifying HIV sequences using HIV primers that

result in a PCR product that comprises the PR gene; (iii) performing PCR using primers that result in PCR products comprising wild type or serine at codon 88 and mutations at codons 63, 77 and/or 46 or a combination thereof; and 5 (iv) determining, via the products of PCR, the presence or absence of a serine residue at codon 88 and the presence or absence of mutations at codons 63, 77 and/or 46 or a combination thereof.

10 Another preferred, non-limiting, specific embodiment of the invention is as follows: A method of evaluating the effectiveness of PRI therapy of a patient comprising (i) collecting a biological sample from an HIV-infected patient; (ii) purifying and converting the viral RNA to 15 cDNA and amplifying HIV sequences using HIV primers that result in a PCR product that comprises the PR gene; (iii) performing PCR using primers that result in PCR products comprising wild type or serine at codon 88 and mutations at codons 63, 77, 46, 10, 20, and/or 36 or a combination thereof; and (iv) determining, via the products of PCR, the presence or absence of a serine residue at codon 88 and the presence or absence of mutations at codons 63, 77, 20 46, 10, 20, and/or 36 or a combination thereof.

25 The presence of the mutation at codon 88 to a serine of HIV PR indicates that the effectiveness of the current or prospective PRI therapy may require alteration, since as shown by this invention mutation at codon 88 to a serine residue increases the susceptibility to amprenavir. Using 30 the methods of this invention, changes in the PRI therapy would be indicated.

The presence of the mutation at codon 88 to a serine of alone or in combination with mutations at condons 63, 77, 46, 10, 20, and/or 36 or a combination thereof of HIV PR indicates that the effectiveness of the current or

5 prospective PRI therapy may require alteration, since as shown by this invention a mutation at codon 88 to a serine residue alone increases the susceptibility to amprenavir and a mutation at codon 88 to a serine residue in combination with mutations at condons 63, 77, 46, 10, 20,

10 and/or 36 or a combination increases the susceptibility to amprenavir but also reduces the susceptibility to nelfinavir and indinavir. Using the methods of this invention, changes in the PRI therapy would be indicated.

15 Another preferred, non-limiting, specific embodiment of the invention is as follows: a method of evaluating the effectiveness of antiretroviral therapy of an HIV-infected patient comprising: (a) collecting a biological sample from an HIV-infected patient; and (b) determining whether the biological sample comprises nucleic acid encoding HIV protease having a mutation at codon 88 to serine. Using the phenotypic susceptibility assay, it was observed that the presence of the mutation at codon 88 to serine of HIV PR causes a an increase in amprenavir susceptibility.

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25 Another preferred, non-limiting, specific embodiment of the invention is as follows: a method of evaluating the effectiveness of antiretroviral therapy of an HIV-infected patient comprising: (a) collecting a biological sample from an HIV-infected patient; and (b) determining whether the biological sample comprises nucleic acid encoding HIV protease having a mutation at codon 88 to serine and

additional mutation(s) at codons 63 and/or 77 or a combination thereof. Using the phenotypic susceptibility assay, it was observed that the presence of the mutation at codon 88 to serine of HIV PR causes an increase in 5 amprenavir susceptibility and the presence of the mutations at codon 88 to serine in combination with a mutation at codon(s) 63 and/or 77 or a combination thereof of HIV PR causes a decrease in nelfinavir and indinavir susceptibility while increasing amprenavir susceptibility.

10

Another preferred, non-limiting, specific embodiment of the invention is as follows: a method of evaluating the effectiveness of antiretroviral therapy of an HIV-infected patient comprising: (a) collecting a biological sample 15 from an HIV-infected patient; and (b) determining whether the biological sample comprises nucleic acid encoding HIV protease having a mutation at codon 88 to serine and additional mutation(s) at codons 63, 77 and/or 46 or a combination thereof. Using the phenotypic susceptibility 20 assay, it was observed that the presence of the mutation at codon 88 to serine of HIV PR causes an increase in amprenavir susceptibility and the presence of the mutations at codon 88 to serine in combination with a mutation at codon(s) 46, 63 and/or 77 or a combination 25 thereof of HIV PR causes a decrease in nelfinavir and indinavir susceptibility while increasing amprenavir susceptibility.

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Another preferred, non-limiting, specific embodiment of the invention is as follows: a method of evaluating the effectiveness of antiretroviral therapy of an HIV-infected patient comprising: (a) collecting a biological sample

from an HIV-infected patient; and (b) determining whether the biological sample comprises nucleic acid encoding HIV protease having a mutation at codon 88 to serine and additional mutation(s) at codons 63, 77, 46, 10, 20 and/or 5 36 or a combination thereof. Using the phenotypic susceptibility assay, it was observed that the presence of the mutation at codon 88 to serine of HIV PR causes an increase in amprenavir susceptibility and the presence of the mutations at codon 88 to serine in combination with a 10 mutation at codon(s) 63, 77, 46, 10, 20 and/or 36 or a combination thereof of HIV PR causes a decrease in nelfinavir and indinavir susceptibility while increasing amprenavir susceptibility.

15 This invention also provides the means and methods to use the resistance test vector comprising an HIV gene and further comprising a PR mutation for drug screening. More particularly, the invention describes the resistance test vector comprising the HIV protease having a mutation at 20 codon 88 to a serine alone or in combination with mutations at codons 10, 20, 36, 46, 63 and/or 77 or a combination thereof for drug screening. The invention further relates to novel vectors, host cells and 25 compositions for isolation and identification of the HIV-1 protease inhibitor resistant mutant and using such vectors, host cells and compositions to carry out anti-viral drug screening. This invention also relates to the screening of candidate drugs for their capacity to inhibit said mutant.

30 This invention provides a method for identifying a compound which is capable of affecting the function of the

protease of HIV-1 comprising contacting the compound with the polypeptide(s) comprising all or part of the HIV-1 protease, wherein codon 88 is changed to a serine residue, wherein a positive binding indicates that the compound is 5 capable of affecting the function of said protease.

This invention also provides a method for assessing the viral fitness of patient's virus comprising: (a) determining the luciferase activity in the absence of drug 10 for the reference control using the susceptibility test described above; (b) determining the luciferase activity in the absence of drug for the patient virus sample using the susceptibility test described above; and (c) comparing the luciferase activity determined in step (b) with the 15 luciferase activity determined in step (a), wherein a decrease in luciferase activity indicates a reduction in viral fitness of the patient's virus.

If a resistance test vector is constructed using a patient 20 derived segment from a patient virus which is unfit, and the fitness defect is due to genetic alterations in the patient derived segment, then the virus produced from cells transfected with the resistance test vector will produce luciferase more slowly. This defect will be 25 manifested as reduced luciferase activity (in the absence of drug) compared to the drug sensitive reference control, and may be expressed as a percentage of the control.

In a further embodiment of the invention, PCR based 30 assays, including phenotypic and genotypic assays, may be used to detect mutations at positions 20 and 88 of HIV PR, which correlate with a reduction in viral fitness and

immunological response.

It is a further embodiment of this invention to provide a means and method for measuring replication fitness for 5 viruses, including, but not limited to human immunodeficiency virus (HIV), hepadnaviruses (human hepatitis B virus), flaviviruses (human hepatitis C virus) and herpesviruses (human cytomegalovirus).

10 This invention further relates to a means and method for measuring the replication fitness of HIV-1 that exhibits reduced drug susceptibility to reverse transcriptase inhibitors and protease inhibitors.

15 In a further embodiment of the invention , a means and methods are provided for measuring replication fitness for other classes of inhibitors of HIV-1 replication, including, but not limited to integration, virus assembly, and virus attachment and entry.

20 This invention relates to a means and method for identifying mutations in protease or reverse transcriptase that alter replication fitness.

25 In a further embodiment of the invention , a means and methods are provided for identifying mutations that alter replication fitness for other components of HIV-1 replication, including, but not limited to integration, virus assembly, and virus attachment and entry.

This invention also relates to a means and method for quantifying the affect that specific mutations in protease or reverse transcriptase have on replication fitness.

5 In a further embodiment of the invention , a means and method are provided for quantifying the affect that specific protease and reverse transcriptase mutations have on replication fitness in other viral genes involved in HIV-1 replication, including, but not limited to the gag, 10 pol, and envelope genes.

This invention also relates to the high incidence of patient samples with reduced replication fitness.

15 This invention relates to the correlation between reduced drug susceptibility and reduced replication fitness.

This invention further relates to the occurrence of viruses with reduced fitness in patients receiving 20 protease inhibitor and/or reverse transcriptase inhibitor treatment.

This invention further relates to the incidence of patient samples with reduced replication fitness in which the 25 reduction in fitness is due to altered protease processing of the gag polyprotein (p55).

This invention further relates to the incidence of protease mutations in patient samples that exhibit low, 30 moderate or normal (wildtype) replication fitness.

This invention further relates to protease mutations that are frequently observed, either alone or in combination, in viruses that exhibit reduced replication capacity.

5 This invention also relates to the incidence of patient samples with reduced replication fitness in which the reduction in fitness is due to altered reverse transcriptase activity. This invention relates to the occurrence of viruses with reduced replication fitness in patients failing antiretroviral drug treatment. This invention further relates to a means and method for using replication fitness measurements to guide the treatment of HIV-1. This invention further relates to a means and method for using replication fitness measurements to guide the treatment of patients failing antiretroviral drug treatment. This invention further relates to the means and methods for using replication fitness measurements to guide the treatment of patients newly infected with HIV-1.

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This invention, provides the means and methods for using replication fitness measurements to guide the treatment of viral diseases, including, but not limited to HIV-1, hepadnaviruses (human hepatitis B virus), flaviviruses (human hepatitis C virus) and herpesviruses (human cytomegalovirus).

In a further embodiment, the invention provides a method for determining replication capacity for a patient's virus comprising:

30 (a) introducing a resistance test vector comprising a patient derived segment and an indicator gene into a host cell;

- (b) culturing the host cell from (a);
- (c) harvesting viral particles from step (b) and infecting target host cells;

5

- (d) measuring expression of the indicator gene in the target host cell, wherein the expression of the indicator gene is dependent upon the patient-derived segment;

10

- (e) comparing the expression of the indicator gene from (d) with the expression of the indicator gene measured when steps (a) through (d) are carried out in a control resistance test vector; and

15

- (f) normalizing the expression of the indicator gene by measuring an amount of virus in step (c).

20 As used herein, "patient-derived segment" encompasses segments derived from human and various animal species. Such species include, but are not limited to chimpanzees, horses, cattles, cats and dogs.

25 Patient-derived segments can also be incorporated into resistance test vectors using any of several alternative cloning techniques as set forth in detail in US Patent Number 5,837,464 (International Publication Number WO 97/27319) which is hereby incorporated by reference. For

30 example, cloning via the introduction of class II restriction sites into both the plasmid backbone and the patient-derived segments or by uracil DNA glycosylase primer cloning.

The patient-derived segment may be obtained by any method of molecular cloning or gene amplification, or modifications thereof, by introducing patient sequence acceptor sites, as described below, at the ends of the 5 patient-derived segment to be introduced into the resistance test vector. For example, in a gene amplification method such as PCR, restriction sites corresponding to the patient-sequence acceptor sites can be incorporated at the ends of the primers used in the PCR 10 reaction. Similarly, in a molecular cloning method such as cDNA cloning, said restriction sites can be incorporated at the ends of the primers used for first or second strand cDNA synthesis, or in a method such as primer-repair of DNA, whether cloned or uncloned DNA, said 15 restriction sites can be incorporated into the primers used for the repair reaction. The patient sequence acceptor sites and primers are designed to improve the representation of patient-derived segments. Sets of resistance test vectors having designed patient sequence 20 acceptor sites provide representation of patient-derived segments that may be underrepresented in one resistance test vector alone.

"Resistance test vector" means one or more vectors which 25 taken together contain DNA comprising a patient-derived segment and an indicator gene. Resistance test vectors are prepared as described in US Patent Number 5,837,464 (International Publication Number WO 97/27319), which is hereby incorporated by reference, by introducing patient 30 sequence acceptor sites, amplifying or cloning patient-derived segments and inserting the amplified or cloned sequences precisely into indicator gene viral

vectors at the patient sequence acceptor sites. Alternatively, a resistance test vector (also referred to as a resistance test vector system) is prepared by introducing patient sequence acceptor sites into a 5 packaging vector, amplifying or cloning patient-derived segments and inserting the amplified or cloned sequences precisely into the packaging vector at the patient sequence acceptor sites and co-transfected this packaging vector with an indicator gene viral vector.

10

"Indicator or indicator gene," as described in US Patent Number 5,837,464 (International Publication Number WO 97/27319) refers to a nucleic acid encoding a protein, DNA or RNA structure that either directly or through a 15 reaction gives rise to a measurable or noticeable aspect, e.g. a color or light of a measurable wavelength or in the case of DNA or RNA used as an indicator a change or generation of a specific DNA or RNA structure. Preferred examples of an indicator gene is the *E. coli* lacZ gene 20 which encodes beta-galactosidase, the luc gene which encodes luciferase either from, for example, *Photinus pyralis* (the firefly) or *Renilla reniformis* (the sea pansy), the *E. coli* phoA gene which encodes alkaline phosphatase, green fluorescent protein and the bacterial 25 CAT gene which encodes chloramphenicol acetyltransferase. The indicator or indicator gene may be functional or non-functional as described in US Patent Number 5,837,464 (International Publication Number WO 97/27319).

30 The phenotypic drug susceptibility and resistance tests of this invention may be carried out in one or more host cells as described in US Patent Number 5,837,464

(International Publication Number WO 97/27319) which is incorporated herein by reference. Viral drug susceptibility is determined as the concentration of the anti-viral agent at which a given percentage of indicator gene expression is inhibited (e.g. the IC50 for an anti-viral agent is the concentration at which 50% of indicator gene expression is inhibited). A standard curve for drug susceptibility of a given anti-viral drug can be developed for a viral segment that is either a standard laboratory viral segment or from a drug-naive patient (i.e. a patient who has not received any anti-viral drug) using the method described in the aforementioned patent. Correspondingly, viral drug resistance is a decrease in viral drug susceptibility for a given patient compared to such a given standard or when making one or more sequential measurements in the same patient over time, as determined by decreased susceptibility in virus from later time points compared to that from earlier time points.

The antiviral drugs being added to the test system are added at selected times depending upon the target of the antiviral drug. For example, in the case of HIV protease inhibitors, including saquinavir, ritonavir, indinavir, nelfinavir and amprenavir, they are added to packaging host cells at the time of or shortly after their transfection with a resistance test vector, at an appropriate range of concentrations. HIV reverse transcriptase inhibitors, including AZT, ddI, ddC, d4T, 3TC, abacavir, nevirapine, delavirdine and efavirenz are added to target host cells at the time of or prior to infection by the resistance test vector viral particles, at an appropriate range of concentration. Alternatively,

the antiviral drugs may be present throughout the assay. The test concentration is selected from a range of concentrations which is typically between about  $8 \times 10^{-6}$   $\mu\text{M}$  and about 2mM and more specifically for each of the 5 following drugs: saquinavir, indinavir, nelfinavir and amprenavir, from about  $2.3 \times 10^{-5}$   $\mu\text{M}$  to about 1.5  $\mu\text{M}$  and ritonavir, from about  $4.5 \times 10^{-5}$   $\mu\text{M}$  to about 3  $\mu\text{M}$ .

In another embodiment of this invention, a candidate PRI 10 antiretroviral compound is tested in the phenotypic drug susceptibility and resistance test using the resistance test vector comprising PR having a mutation at codon 88 to a serine. The candidate antiviral compound is added to the test system at an appropriate range of concentrations and 15 at the transfection step. Alternatively, more than one candidate antiviral compound may be tested or a candidate antiviral compound may be tested in combination with an approved antiviral drug such as AZT, ddI, ddC, d4T, 3TC, abacavir, delavirdine, nevirapine, efavirenz, saquinavir, 20 ritonavir, indinavir, nelfinavir, amprenavir, or a compound which is undergoing clinical trials such as adefovir and ABT-378. The effectiveness of the candidate antiviral will be evaluated by measuring the expression or 25 inhibition of the indicator gene. In another aspect of this embodiment, the drug susceptibility and resistance test may be used to screen for viral mutants. Following the identification of mutants resistant to either known 30 antiretrovirals or candidate antiretrovirals the resistant mutants are isolated and the DNA is analyzed. A library of viral resistant mutants can thus be assembled enabling the screening of candidate PRI antiretrovirals, alone or in combination. This will enable one of ordinary skill to

identify effective PRI antiretrovirals and design effective therapeutic regimens.

5 In another embodiment of this invention, a method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient is provided comprising:  
10 (a) collecting a biological sample from the HIV-infected patient;  
(b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 or codon 90; and  
(c) determining changes in susceptibility to protease inhibitors.

15 In another embodiment of this invention, the method is provided, wherein step (c) determines changes in susceptibility to saquinavir.

20 In another embodiment of this invention, the method is provided, wherein the mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

25 In another embodiment of this invention, the method is provided, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V).

30 In another embodiment of this invention, the method is provided, wherein the mutation at codon 90 codes for methionine (M).

In another embodiment of this invention, the method is provided, wherein the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

5 In another embodiment of this invention, a method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound is provided comprising:

10 (a) introducing a resistance test vector comprising a patient-derived segment having nucleic acid encoding HIV protease with a mutation at codon 82 or codon 90 and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

15 (c) measuring the indicator gene in a target host cell; and

(d) comparing the measurement of the indicator gene from step (c) with the measurement of the indicator gene measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

20 wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

25 In another embodiment of this invention, a resistance test vector comprising an HIV patient-derived segment further comprising protease having a mutation at codon 82 or codon 90 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient-derived segment.

30 In another embodiment of this invention, the resistance test vector is provided, wherein the patient-derived

segment having a mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

5 In another embodiment of this invention, the resistance test vector of is provided , wherein the patient-derived segment having a mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V).

10 In another embodiment of this invention, the resistance test vector is provided , wherein the patient-derived segment having a mutation at codon 90 codes for methionine (M) .

15 In yet another embodiment of this invention, the resistance test vector is provided, wherein the patient-derived segment having a mutation at codon 90 is a substitution of methionine (M) for leucine (L).

20 In another embodiment of this invention, a method for determining replication capacity for a patient's virus is provided comprising:

25 (a) introducing a resistance test vector comprising a patient-derived segment and an indicator gene into a host cell;

(b) culturing the host cell from (a);

(c) harvesting viral particles from step (b) and infecting target host cells;

30 (d) measuring expression of the indicator gene in the target host cell, wherein the expression of the indicator gene is dependent upon the patient-derived segment; and

(e) comparing the expression of the indicator gene from (d) with the expression of the indicator gene measured when steps (a) through (d) are carried out in a control resistance test vector.

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In another embodiment of this invention, the method further comprises the step of:

(f) normalizing the expression of the indicator gene by measuring an amount of virus in step (c).

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In another embodiment of this invention, the method is provided wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having a mutation at codon 66.

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In another embodiment of this invention, the method is provided wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having a mutation at codon 154.

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In another embodiment of this invention, the method is provided wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having mutations at codon 66 and codon 153.

25

In another embodiment of this invention, the method is provided wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having mutations at codon 66 and codon 154.

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- 60 -

In another embodiment of this invention, a method is provided of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

- 5 (a) collecting a biological sample from the HIV-infected patient;
- (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71, 64, 93, 23, 58, and 36; and
- 10 (c) determining a change in susceptibility to a protease inhibitor.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

25 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

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5 The structure, life cycle and genetic elements of the viruses which could be tested in the drug susceptibility and resistance test of this invention would be known to one of ordinary skill in the art. It is useful to the practice of this invention, for example, to understand the  
10 life cycle of a retrovirus, as well as the viral genes required for retrovirus rescue and infectivity. Retrovirally infected cells shed a membrane virus containing a diploid RNA genome. The virus, studded with an envelope glycoprotein (which serves to determine the  
15 host range of infectivity), attaches to a cellular receptor in the plasma membrane of the cell to be infected. After receptor binding, the virus is internalized and uncoated as it passes through the cytoplasm of the host cell. Either on its way to the  
20 nucleus or in the nucleus, the reverse transcriptase molecules resident in the viral core drive the synthesis of the double-stranded DNA provirus, a synthesis that is primed by the binding of a tRNA molecule to the genomic viral RNA. The double-stranded DNA provirus is  
25 subsequently integrated in the genome of the host cell, where it can serve as a transcriptional template for both mRNAs encoding viral proteins and virion genomic RNA, which will be packaged into viral core particles. On their way out of the infected cell, core particles move  
30 through the cytoplasm, attach to the inside of the plasma membrane of the newly infected cell, and bud, taking with them tracts of membrane containing the virally encoded envelope glycoprotein gene product. This cycle of  
35 infection - reverse transcription, transcription, translation, virion assembly, and budding - repeats itself

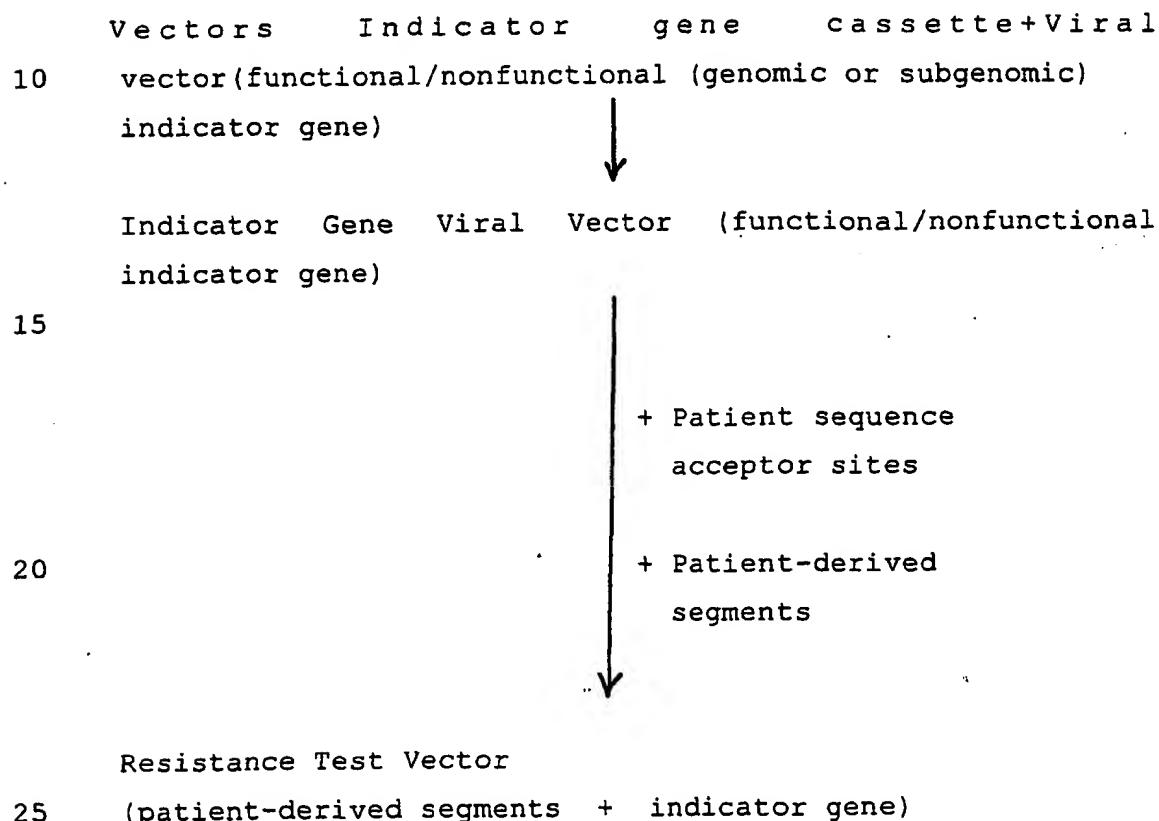
5 over and over again as infection spreads.

The viral RNA and, as a result, the proviral DNA encode several cis-acting elements that are vital to the successful completion of the viral lifecycle. The virion 10 RNA carries the viral promoter at its 3' end. Replicative acrobatics place the viral promoter at the 5' end of the proviral genome as the genome is reverse transcribed. Just 3' to the 5' retroviral LTR lies the viral packaging site. The retroviral lifecycle requires the presence of 15 virally encoded transacting factors. The viral-RNA-dependent DNA polymerase (*pol*)-reverse transcriptase is also contained within the viral core and is vital to the viral life cycle in that it is responsible for the conversion of the genomic RNA to the integrative 20 intermediate proviral DNA. The viral envelope glycoprotein, *env*, is required for viral attachment to the uninfected cell and for viral spread. There are also transcriptional trans-activating factors, so called transactivators, that can serve to modulate the level of 25 transcription of the integrated parental provirus. Typically, replication-competent (non-defective) viruses are self-contained in that they encode all of these trans-acting factors. Their defective counterparts are not self-contained.

30 In the case of a DNA virus, such as a hepadnavirus, understanding the life cycle and viral genes required for infection is useful to the practice of this invention. The process of HBV entry has not been well defined. 35 Replication of HBV uses an RNA intermediate template. In the infected cell the first step in replication is the

5 conversion of the asymmetric relaxed circle DNA (rc-DNA) to covalently closed circle DNA (cccDNA). This process, which occurs within the nucleus of infected liver cells, involves completion of the DNA positive-strand synthesis and ligation of the DNA ends. In the second step, the  
10 cccDNA is transcribed by the host RNA polymerase to generate a 3.5 kB RNA template (the pregenome). This pregenome is complexed with protein in the viral core. The third step involves the synthesis of the first negative-sense DNA strand by copying the pregenomic RNA using the virally encoded P protein reverse transcriptase.  
15 The P protein also serves as the minus strand DNA primer. Finally, the synthesis of the second positive-sense DNA strand occurs by copying the first DNA strand, using the P protein DNA polymerase activity and an oligomer of viral RNA as primer. The pregenome also transcribes mRNA for  
20 the major structural core proteins.

5 The following flow chart illustrates certain of the various vectors and host cells which may be used in this invention. It is not intended to be all inclusive.



### Host Cells

30 Packaging Host Cell - transfected with packaging  
expression vectors

Resistance Test Vector Host Cell - a packaging host cell transfected with a resistance test vector

35 Target Host Cell - a host cell to be infected by a

5      resistance test vector viral particle produced by the  
resistance test vector host cell

***Resistance Test Vector***

"Resistance test vector" means one or more vectors which  
10     taken together contain DNA or RNA comprising a  
patient-derived segment and an indicator gene. In the  
case where the resistance test vector comprises more than  
one vector the patient-derived segment may be contained in  
one vector and the indicator gene in a different vector.  
15     Such a resistance test vector comprising more than one  
vector is referred to herein as a resistance test vector  
system for purposes of clarity but is nevertheless  
understood to be a resistance test vector. The DNA or RNA  
of a resistance test vector may thus be contained in one  
20     or more DNA or RNA molecules. In one embodiment, the  
resistance test vector is made by insertion of a  
patient-derived segment into an indicator gene viral  
vector. In another embodiment, the resistance test vector  
is made by insertion of a patient-derived segment into a  
25     packaging vector while the indicator gene is contained in  
a second vector, for example an indicator gene viral  
vector. As used herein, "patient-derived segment" refers  
to one or more viral segments obtained directly from a  
patient using various means, for example, molecular  
30     cloning or polymerase chain reaction (PCR) amplification  
of a population of patient-derived segments using viral  
DNA or complementary DNA (cDNA) prepared from viral RNA,  
present in the cells (e.g. peripheral blood mononuclear  
cells, PBMC), serum or other bodily fluids of infected  
35     patients. When a viral segment is "obtained directly"  
from a patient it is obtained without passage of the virus

5 through culture, or if the virus is cultured, then by a minimum number of passages to essentially eliminate the selection of mutations in culture. The term "viral segment" refers to any functional viral sequence or viral gene encoding a gene product (e.g., a protein) that is the  
10 target of an anti-viral drug. The term "functional viral sequence" as used herein refers to any nucleic acid sequence (DNA or RNA) with functional activity such as enhancers, promoters, polyadenylation sites, sites of action of trans-acting factors, such as tar and RRE,  
15 packaging sequences, integration sequences, or splicing sequences. If a drug were to target more than one functional viral sequence or viral gene product then patient-derived segments corresponding to each said viral gene would be inserted in the resistance test vector. In  
20 the case of combination therapy where two or more anti-virals targeting two different functional viral sequences or viral gene products are being evaluated, patient-derived segments corresponding to each functional viral sequence or viral gene product would be inserted in  
25 the resistance test vector. The patient-derived segments are inserted into unique restriction sites or specified locations, called patient sequence acceptor sites, in the indicator gene viral vector or for example, a packaging vector depending on the particular construction being used  
30 as described herein.

As used herein, "patient-derived segment" encompasses segments derived from human and various animal species. Such species include, but are not limited to chimpanzees, horses, cattles, cats and dogs.  
35

5 Patient-derived segments can also be incorporated into  
resistance test vectors using any of several alternative  
cloning techniques. For example, cloning via the  
introduction of class II restriction sites into both the  
plasmid backbone and the patient-derived segments or by  
10 uracil DNA glycosylase primer cloning (refs).

The patient-derived segment may be obtained by any method  
of molecular cloning or gene amplification, or  
modifications thereof, by introducing patient sequence  
15 acceptor sites, as described below, at the ends of the  
patient-derived segment to be introduced into the  
resistance test vector. For example, in a gene  
amplification method such as PCR, restriction sites  
corresponding to the patient-sequence acceptor sites can  
20 be incorporated at the ends of the primers used in the PCR  
reaction. Similarly, in a molecular cloning method such  
as cDNA cloning, said restriction sites can be  
incorporated at the ends of the primers used for first or  
second strand cDNA synthesis, or in a method such as  
25 primer-repair of DNA, whether cloned or uncloned DNA, said  
restriction sites can be incorporated into the primers  
used for the repair reaction. The patient sequence  
acceptor sites and primers are designed to improve the  
representation of patient-derived segments. Sets of  
30 resistance test vectors having designed patient sequence  
acceptor sites provide representation of patient-derived  
segments that would be underrepresented in one resistance  
test vector alone.

35 Resistance test vectors are prepared by modifying an  
indicator gene viral vector (described below) by

5 introducing patient sequence acceptor sites, amplifying or cloning patient-derived segments and inserting the amplified or cloned sequences precisely into indicator gene viral vectors at the patient sequence acceptor sites.

10 The resistance test vectors are constructed from indicator gene viral vectors which are in turn derived from genomic viral vectors or subgenomic viral vectors and an indicator gene cassette, each of which is described below. Resistance test vectors are then introduced into a host cell. Alternatively, a resistance test vector (also 15 referred to as a resistance test vector system) is prepared by introducing patient sequence acceptor sites into a packaging vector, amplifying or cloning patient-derived segments and inserting the amplified or cloned sequences precisely into the packaging vector at 20 the patient sequence acceptor sites and co-transfected this packaging vector with an indicator gene viral vector.

25 In one preferred embodiment, the resistance test vector may be introduced into packaging host cells together with packaging expression vectors, as defined below, to produce resistance test vector viral particles that are used in drug resistance and susceptibility tests that are referred to herein as a "particle-based test." In an alternative preferred embodiment, the resistance test vector may be 30 introduced into a host cell in the absence of packaging expression vectors to carry out a drug resistance and susceptibility test that is referred to herein as a "non-particle-based test." As used herein a "packaging expression vector" provides the factors, such as packaging 35 proteins (e.g. structural proteins such as core and envelope polypeptides), transacting factors, or genes

5 required by replication-defective retrovirus or hepadnavirus. In such a situation, a replication-competent viral genome is enfeebled in a manner such that it cannot replicate on its own. This means that, although the packaging expression vector can 10 produce the trans-acting or missing genes required to rescue a defective viral genome present in a cell containing the enfeebled genome, the enfeebled genome cannot rescue itself.

15 ***Indicator or Indicator Gene***

"Indicator or indicator gene" refers to a nucleic acid encoding a protein, DNA or RNA structure that either directly or through a reaction gives rise to a measurable or noticeable aspect, e.g. a color or light of a measurable wavelength or in the case of DNA or RNA used as 20 an indicator a change or generation of a specific DNA or RNA structure. Preferred examples of an indicator gene is the *E. coli lacZ* gene which encodes beta-galactosidase, the *luc* gene which encodes luciferase either from, for 25 example, *Photinus pyralis* (the firefly) or *Renilla reniformis* (the sea pansy), the *E. coli phoA* gene which encodes alkaline phosphatase, green fluorescent protein and the bacterial CAT gene which encodes chloramphenicol acetyltransferase. Additional preferred examples of an 30 indicator gene are secreted proteins or cell surface proteins that are readily measured by assay, such as radioimmunoassay (RIA), or fluorescent activated cell sorting (FACS), including, for example, growth factors, cytokines and cell surface antigens (e.g. growth hormone, 35 IL-2 or CD4, respectively). "Indicator gene" is understood to also include a selection gene, also referred

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5 to as a selectable marker. Examples of suitable selectable markers for mammalian cells are dihydrofolate reductase (DHFR), thymidine kinase, hygromycin, neomycin, zeocin or *E. coli* gpt. In the case of the foregoing examples of indicator genes, the indicator gene and the 10 patient-derived segment are discrete, i.e. distinct and separate genes. In some cases a patient-derived segment may also be used as an indicator gene. In one such embodiment in which the patient-derived segment corresponds to more than one viral gene which is the 15 target of an anti-viral, one of said viral genes may also serve as the indicator gene. For example, a viral protease gene may serve as an indicator gene by virtue of its ability to cleave a chromogenic substrate or its ability to activate an inactive zymogen which in turn 20 cleaves a chromogenic substrate, giving rise in each case to a color reaction. In all of the above examples of indicator genes, the indicator gene may be either "functional" or "non-functional" but in each case the expression of the indicator gene in the target cell is 25 ultimately dependent upon the action of the patient-derived segment.

Functional Indicator Gene

In the case of a "functional indicator gene" the indicator 30 gene may be capable of being expressed in a "packaging host cell/resistance test vector host cell" as defined below, independent of the patient-derived segment, however the functional indicator gene could not be expressed in the target host cell, as defined below, 35 without the production of functional resistance test vector particles and their effective infection of the

5 target host cell. In one embodiment of a functional indicator gene, the indicator gene cassette, comprising control elements and a gene encoding an indicator protein, is inserted into the indicator gene viral vector with the same or opposite transcriptional orientation as the native 10 or foreign enhancer/promoter of the viral vector. One example of a functional indicator gene in the case of HIV or HBV, places the indicator gene and its promoter (a CMV IE enhancer/promoter) in the same or opposite transcriptional orientation as the HIV-LTR or HBV 15 enhancer-promoter, respectively, or the CMV IE enhancer/promoter associated with the viral vector.

Non-Functional Indicator Gene

20 Alternatively the indicator gene, may be "non-functional" in that the indicator gene is not efficiently expressed in a packaging host cell transfected with the resistance test vector, which is then referred to a resistance test vector host cell, until it is converted into a functional 25 indicator gene through the action of one or more of the patient-derived segment products. An indicator gene is rendered non-functional through genetic manipulation according to this invention.

30 1. Permuted Promoter In one embodiment an indicator gene is rendered non-functional due to the location of the promoter, in that, although the promoter is in the same transcriptional orientation as the indicator gene, it follows rather than precedes the indicator gene coding sequence. This misplaced promoter is referred to as a 35 "permuted promoter." In addition to the permuted promoter the orientation of the non-functional indicator gene is

5 opposite to that of the native or foreign promoter/enhancer of the viral vector. Thus the coding sequence of the non-functional indicator gene can neither be transcribed by the permuted promoter nor by the viral promoters. The non-functional indicator gene and its  
10 permuted promoter is rendered functional by the action of one or more of the viral proteins. One example of a non-functional indicator gene with a permuted promoter in the case of HIV, places a T7 phage RNA polymerase promoter (herein referred to as T7 promoter) promoter in the 5' LTR in the same transcriptional orientation as the indicator gene. The indicator gene cannot be transcribed by the T7 promoter as the indicator gene cassette is positioned upstream of the T7 promoter. The non-functional indicator gene in the resistance test vector is converted into a  
15 functional indicator gene by reverse transcriptase upon infection of the target cells, resulting from the repositioning of the T7 promoter, by copying from the 5' LTR to the 3' LTR, relative to the indicator gene coding region. Following the integration of the repaired  
20 indicator gene into the target cell chromosome by HIV integrase, a nuclear T7 RNA polymerase expressed by the target cell transcribes the indicator gene. One example of a non-functional indicator gene with a permuted promoter in the case of HBV, places an enhancer-promoter region downstream or 3' of the indicator gene both having  
25 the same transcriptional orientation. The indicator gene cannot be transcribed by the enhancer-promoter as the indicator gene cassette is positioned upstream. The non-functional indicator gene in the resistance test vector is converted into a functional indicator gene by  
30 reverse transcription and circularization of the HBV  
35

5 indicator gene viral vector by the repositioning of the  
enhancer-promoter upstream relative to the indicator gene  
coding region.

A permuted promoter may be any eukaryotic or prokaryotic  
10 promoter which can be transcribed in the target host cell.  
Preferably the promoter will be small in size to enable  
insertion in the viral genome without disturbing viral  
replication. More preferably, a promoter that is small in  
15 size and is capable of transcription by a single subunit  
RNA polymerase introduced into the target host cell, such  
as a bacteriophage promoter, will be used. Examples of  
such bacteriophage promoters and their cognate RNA  
polymerases include those of phages T7, T3 and Sp6. A  
nuclear localization sequence (NLS) may be attached to the  
20 RNA polymerase to localize expression of the RNA  
polymerase to the nucleus where they may be needed to  
transcribed the repaired indicator gene. Such an NLS may  
be obtained from any nuclear-transported protein such as  
the SV40 T antigen. If a phage RNA polymerase is  
25 employed, an internal ribosome entry site (IRES) such as  
the EMC virus 5' untranslated region (UTR) may be added in  
front of the indicator gene, for translation of the  
transcripts which are generally uncapped. In the case of  
HIV, the permuted promoter itself can be introduced at any  
30 position within the 5' LTR that is copied to the 3' LTR  
during reverse transcription so long as LTR function is  
not disrupted, preferably within the U5 and R portions of  
the LTR, and most preferably outside of functionally  
important and highly conserved regions of U5 and R. In  
35 the case of HBV, the permuted promoter can be placed at  
any position that does not disrupt the cis acting elements

5 that are necessary for HBV DNA replication. Blocking sequences may be added at the ends of the resistance test vector should there be inappropriate expression of the non-functional indicator gene due to transfection artifacts (DNA concatenation). In the HIV example of the 10 permuted T7 promoter given above, such a blocking sequence may consist of a T7 transcriptional terminator, positioned to block readthrough transcription resulting from DNA concatenation, but not transcription resulting from repositioning of the permuted T7 promoter from the 5' LTR 15 to the 3' LTR during reverse transcription.

2. Permuted Coding Region In a second embodiment, an indicator gene is rendered non-functional due to the relative location of the 5' and 3' coding regions of the 20 indicator gene, in that, the 3' coding region precedes rather than follows the 5' coding region. This misplaced coding region is referred to as a "permuted coding region." The orientation of the non-functional indicator 25 gene may be the same or opposite to that of the native or foreign promoter/enhancer of the viral vector, as mRNA coding for a functional indicator gene will be produced in the event of either orientation. The non-functional indicator gene and its permuted coding region is rendered 30 functional by the action of one or more of the patient-derived segment products. A second example of a non-functional indicator gene with a permuted coding region in the case of HIV, places a 5' indicator gene coding region with an associated promoter in the 3' LTR U3 35 region and a 3' indicator gene coding region in an upstream location of the HIV genome, with each coding region having the same transcriptional orientation as the

5     viral LTRs.    In both examples, the 5' and 3' coding  
regions may also have associated splice donor and acceptor  
sequences, respectively, which may be heterologous or  
artificial splicing signals.  The indicator gene cannot be  
functionally transcribed either by the associated promoter  
10    or viral promoters, as the permuted coding region prevents  
the formation of functionally spliced transcripts.  The  
non-functional indicator gene in the resistance test  
vector is converted into a functional indicator gene by  
reverse transcriptase upon infection of the target cells,  
15    resulting from the repositioning of the 5' and 3'  
indicator gene coding regions relative to one another, by  
copying of the 3' LTR to the 5' LTR.  Following  
transcription by the promoter associated with the 5'  
coding region, RNA splicing can join the 5' and 3' coding  
20    regions to produce a functional indicator gene product.  
One example of a non-functional indicator gene with a  
permuted coding region in the case of HBV, places a 3'  
indicator gene coding region upstream or 5' of the  
enhancer-promoter and the 5' coding region of the  
25    indicator gene.  The transcriptional orientation of the  
indicator gene 5' and 3' coding regions are identical to  
one another, and the same as that of the indicator gene  
viral vector.  However, as the indicator gene 5' and 3'  
coding regions are permuted in the resistance test vectors  
30    (i.e., the 5' coding region is downstream of the 3' coding  
region), no mRNA is transcribed which can be spliced to  
generate a functional indicator gene coding region.  
Following reverse transcription and circularization of the  
indicator gene viral vector, the indicator gene 3' coding  
35    region is positioned downstream or 3' to the  
enhancer-promoter and 5' coding regions thus permitting

5 the transcription of mRNA which can be spliced to generate  
a functional indicator gene coding region.

3. Inverted Intron In a third embodiment, the indicator  
gene is rendered non-functional through use of an  
10 "inverted intron," i.e. an intron inserted into the coding  
sequence of the indicator gene with a transcriptional  
orientation opposite to that of the indicator gene. The  
overall transcriptional orientation of the indicator gene  
cassette including its own, linked promoter, is opposite  
15 to that of the viral control elements, while the  
orientation of the artificial intron is the same as the  
viral control elements. Transcription of the indicator  
gene by its own linked promoter does not lead to the  
production of functional transcripts as the inverted  
20 intron cannot be spliced in this orientation.  
Transcription of the indicator gene by the viral control  
elements does, however, lead to the removal of the  
inverted intron by RNA splicing, although the indicator  
gene is still not functionally expressed as the resulting  
25 transcript has an antisense orientation. Following the  
reverse transcription of this transcript and integration  
of the resultant retroviral DNA, or the circularization of  
hepadnavirus DNA, the indicator gene can be functionally  
transcribed using its own linked promoter as the inverted  
30 intron has been previously removed. In this case, the  
indicator gene itself may contain its own functional  
promoter with the entire transcriptional unit oriented  
opposite to the viral control elements. Thus the  
non-functional indicator gene is in the wrong orientation  
35 to be transcribed by the viral control elements and it  
cannot be functionally transcribed by its own promoter, as

5 the inverted intron cannot be properly excised by  
splicing. However, in the case of a retrovirus and HIV  
specifically and hepadnaviruses, and HBV specifically,  
transcription by the viral promoters (HIV LTR or HBV  
enhancer-promoter) results in the removal of the inverted  
10 intron by splicing. As a consequence of reverse  
transcription of the resulting spliced transcript and the  
integration of the resulting provirus into the host cell  
chromosome or circularization of the HBV vector, the  
indicator gene can now be functionally transcribed by its  
15 own promoter. The inverted intron, consisting of a splice  
donor and acceptor site to remove the intron, is  
preferably located in the coding region of the indicator  
gene in order to disrupt translation of the indicator  
gene. The splice donor and acceptor may be any splice  
20 donor and acceptor. A preferred splice donor-receptor is  
the CMV IE splice donor and the splice acceptor of the  
second exon of the human alpha globin gene ("intron A").

***Indicator Gene Viral Vector - Construction***

25 As used herein, "indicator gene viral vector" refers to a  
vector(s) comprising an indicator gene and its control  
elements and one or more viral genes. The indicator gene  
viral vector is assembled from an indicator gene cassette  
and a "viral vector," defined below. The indicator gene  
30 viral vector may additionally include an enhancer,  
splicing signals, polyadenylation sequences,  
transcriptional terminators, or other regulatory  
sequences. Additionally the indicator gene viral vector  
may be functional or nonfunctional. In the event that the  
35 viral segments which are the target of the anti-viral drug  
are not included in the indicator gene viral vector they

5 are provided in a second vector. An "indicator gene cassette" comprises an indicator gene and control elements. "Viral vector" refers to a vector comprising some or all of the following: viral genes encoding a gene product, control sequences, viral packaging sequences, and  
10 in the case of a retrovirus, integration sequences. The viral vector may additionally include one or more viral segments one or more of which may be the target of an anti-viral drug. Two examples of a viral vector which contain viral genes are referred to herein as an "genomic  
15 viral vector" and a "subgenomic viral vector." A "genomic viral vector" is a vector which may comprise a deletion of a one or more viral genes to render the virus replication incompetent, but which otherwise preserves the mRNA expression and processing characteristics of the complete  
20 virus. In one embodiment for an HIV drug susceptibility and resistance test, the genomic viral vector comprises the HIV *gag-pol*, *vif*, *vpr*, *tat*, *rev*, *vpu*, and *nef* genes (some, most or all of *env* may be deleted). A "subgenomic viral vector" refers to a vector comprising the coding  
25 region of one or more viral genes which may encode the proteins that are the target(s) of the anti-viral drug. In the case of HIV, a preferred embodiment is a subgenomic viral vector comprising the HIV *gag-pol* gene. In the case of HBV a preferred embodiment is a subgenomic viral vector comprising the HBV P gene. In the case of HIV, two examples of proviral clones used for viral vector construction are: HXB2 (Fisher et al., (1986) *Nature*, 320, 367-371) and NL4-3, (Adachi et al., (1986) *J. Virol.*, 59, 284-291). In the case of HBV, a large number of full  
30 length genomic sequences have been characterized and could be used for construction of HBV viral vectors: GenBank  
35

5 Nos. M54923, M38636, J02203 and X59795. The viral coding  
genes may be under the control of a native  
enhancer/promoter or a foreign viral or cellular  
enhancer/promoter. A preferred embodiment for an HIV drug  
susceptibility and resistance test, is to place the  
10 genomic or subgenomic viral coding regions under the  
control of the native enhancer/promoter of the HIV-LTR U3  
region or the CMV immediate-early (IE) enhancer/promoter.  
A preferred embodiment for an HBV drug susceptibility and  
resistance test, is to place the genomic or subgenomic  
15 viral coding regions under the control of the CMV  
immediate-early (IE) enhancer/promoter. In the case of an  
indicator gene viral vector that contains one or more  
viral genes which are the targets or encode proteins which  
are the targets of an anti-viral drug(s) then said vector  
20 contains the patient sequence acceptor sites. The  
patient-derived segments are inserted in the patient  
sequence acceptor site in the indicator gene viral vector  
which is then referred to as the resistance test vector,  
as described above.

25 "Patient sequence acceptor sites" are sites in a vector  
for insertion of patient-derived segments and said sites  
may be: 1) unique restriction sites introduced by  
site-directed mutagenesis into a vector; 2) naturally  
30 occurring unique restriction sites in the vector; or 3)  
selected sites into which a patient-derived segment may be  
inserted using alternative cloning methods (e.g. UDG  
cloning). In one embodiment the patient sequence acceptor  
site is introduced into the indicator gene viral vector.  
35 The patient sequence acceptor sites are preferably located  
within or near the coding region of the viral protein

5 which is the target of the anti-viral drug. The viral  
10 sequences used for the introduction of patient sequence  
acceptor sites are preferably chosen so that no change, or  
a conservative change, is made in the amino acid coding  
sequence found at that position. Preferably the patient  
15 sequence acceptor sites are located within a relatively  
conserved region of the viral genome to facilitate  
introduction of the patient-derived segments. Alternatively,  
20 the patient sequence acceptor sites are located between functionally important genes or regulatory  
25 sequences. Patient-sequence acceptor sites may be located  
at or near regions in the viral genome that are relatively  
conserved to permit priming by the primer used to  
introduce the corresponding restriction site into the  
30 patient-derived segment. To improve the representation of  
patient-derived segments further, such primers may be  
designed as degenerate pools to accommodate viral sequence  
heterogeneity, or may incorporate residues such as  
deoxyinosine (I) which have multiple base-pairing  
35 capabilities. Sets of resistance test vectors having  
patient sequence acceptor sites that define the same or  
overlapping restriction site intervals may be used  
together in the drug resistance and susceptibility tests  
40 to provide representation of patient-derived segments that  
contain internal restriction sites identical to a given  
patient sequence acceptor site, and would thus be  
underrepresented in either resistance test vector alone.

***Host Cells***

45 The resistance test vector is introduced into a host cell.  
35 Suitable host cells are mammalian cells. Preferred host  
cells are derived from human tissues and cells which are

5 the principle targets of viral infection. In the case of HIV these include human cells such as human T cells, monocytes, macrophage, dendritic cells, Langerhans cells, hematopoietic stem cells or precursor cells, and other cells. In the case of HBV, suitable host cells include  
10 hepatoma cell lines (HepG2, Huh 7), primary human hepatocytes, mammalian cells which can be- infected by pseudotyped HBV, and other cells. Human derived host cells will assure that the anti-viral drug will enter the cell efficiently and be converted by the cellular enzymatic machinery into the metabolically relevant form  
15 of the anti-viral inhibitor. Host cells are referred to herein as a "packaging host cells," "resistance test vector host cells," or "target host cells." A "packaging host cell" refers to a host cell that provides the trans-acting factors and viral packaging proteins required  
20 by the replication defective viral vectors used herein, such as the resistance test vectors, to produce resistance test vector viral particles. The packaging proteins may be provided for by the expression of viral genes contained  
25 within the resistance test vector itself, a packaging expression vector(s), or both. A packaging host cell is a host cell which is transfected with one or more packaging expression vectors and when transfected with a resistance test vector is then referred to herein as a "resistance test vector host cell" and is sometimes referred to as a packaging host cell/resistance test vector host cell. Preferred host cells for use as packaging host cells for  
30 HIV include 293 human embryonic kidney cells (293, Graham, F.L. et al., J. Gen Virol. 36: 59, 1977), BOSC23 (Pear et al., Proc. Natl. Acad. Sci. 90, 8392, 1993), tsa54 and  
35 tsa201 cell lines (Heinzel et al., J.Virol. 62,

5 3738,1988), for HBV HepG2 (Galle and Theilmann, L. Arzheim.-Forschy Drug Res. (1990) 40, 1380-1382). (Huh, Ueda, K et al. Virology \*1989) 169, 213-216). A "target host cell" refers to a cell to be infected by resistance test vector viral particles produced by the resistance test vector host cell in which expression or inhibition of the indicator gene takes place. Preferred host cells for use as target host cells include human T cell leukemia cell lines including Jurkat (ATCC T1B-152), H9 (ATCC HTB-176), CEM (ATCC CCL-119), HUT78 (ATCC T1B-161), and derivatives thereof.

10 This invention is illustrated in the Experimental Details section which follows. These sections are set forth to aid in an understanding of the invention but are not intended to, and should not be construed to, limit in any 20 way the invention as set forth in the claims which follow thereafter.

#### Experimental Details

##### 25 General Materials and Methods

Most of the techniques used to construct vectors, and transfect and infect cells, are widely practiced in the art, and most practitioners are familiar with the standard resource materials that describe specific conditions and 30 procedures. However, for convenience, the following paragraphs may serve as a guideline.

As used herein, "replication capacity" is defined herein is a measure of how well the virus replicates. This may 35 also be referred to as viral fitness. In one embodiment, replication capacity can be measured by evaluating the

5 ability of the virus to replicate in a single round of replication.

As used herein, "control resistance test vector" is defined as a resistance test vector comprising a standard 10 viral sequence (for example, HXB2, PNL4-3) and an indicator gene.

As used herein, "normalizing" is defined as standardizing the amount of the expression of indicator gene measured 15 relative to the number of viral particles giving rise to the expression of the indicator gene. For example, normalization is measured by dividing the amount of luciferase activity measured by the number of viral particles measured at the time of infection.

20 "Plasmids" and "vectors" are designated by a lower case p followed by letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed 25 from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

30 Construction of the vectors of the invention employs standard ligation and restriction techniques which are well understood in the art (see Ausubel et al., (1987) Current Protocols in Molecular Biology, Wiley - Interscience or Maniatis et al., (1992) in Molecular 35 Cloning: A laboratory Manual, Cold Spring Harbor Laboratory, N.Y.). Isolated plasmids, DNA sequences, or

5 synthesized oligonucleotides are cleaved, tailored, and religated in the form desired. The sequences of all DNA constructs incorporating synthetic DNA were confirmed by DNA sequence analysis (Sanger et al. (1977) Proc. Natl. Acad. Sci. 74, 5463-5467).

10

"Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences, restriction sites, in the DNA. The various restriction enzymes used herein are commercially available 15 and their reaction conditions, cofactors and other requirements are known to the ordinarily skilled artisan. For analytical purposes, typically 1  $\mu$ g of plasmid or DNA fragment is used with about 2 units of enzyme in about 20  $\mu$ l of buffer solution. Alternatively, an excess of 20 restriction enzyme is used to insure complete digestion of the DNA substrate. Incubation times of about one hour to two hours at about 37°C are workable, although variations can be tolerated. After each incubation, protein is removed by extraction with phenol/chloroform and the 25 nucleic acid recovered from aqueous fractions by precipitation with ethanol. If desired, size separation of the cleaved fragments may be performed by polyacrylamide gel or agarose gel electrophoresis using standard techniques. A general description of size 30 separations is found in Methods of Enzymology 65:499-560 (1980).

35 Restriction cleaved fragments may be blunt ended by treating with the large fragment of E. coli DNA polymerase I (Klenow) in the presence of the four deoxynucleotide triphosphates (dNTPs) using incubation times of about 15

5 to 25 minutes at 20°C in 50 mM Tris (pH 7.6) 50 mM NaCl, 6 mM MgCl<sub>2</sub>, 6 mM DTT and 5-10 mM dNTPs. The Klenow fragment fills in at 5' sticky ends but chews back protruding 3' single strands, even though the four dNTPs are present. If desired, selective repair can be performed by supplying  
10 only one of the dNTPs, or with selected dNTPs, within the limitations dictated by the nature of the sticky ends. After treatment with Klenow, the mixture is extracted with phenol/chloroform and ethanol precipitated. Treatment under appropriate conditions with S1 nuclease or Bal-31  
15 results in hydrolysis of any single-stranded portion.

Ligations are performed in 15-50  $\mu$ l volumes under the following standard conditions and temperatures: 20 mM Tris-Cl pH 7.5, 10 mM MgCl<sub>2</sub>, 10 mM DTT, 33 mg/ml BSA, 10 mM- 50 mM NaCl, and either 40  $\mu$ M ATP, 0.01-0.02 (Weiss) units T4 DNA ligase at 0°C (for "sticky end" ligation) or 1mM ATP, 0.3 - 0.6 (Weiss) units T4 DNA ligase at 14°C (for "blunt end" ligation). Intermolecular "sticky end" ligations are usually performed at 33-100  $\mu$ g/ml total DNA  
25 concentrations (5-100 mM total end concentration). Intermolecular blunt end ligations (usually employing a 10-30 fold molar excess of linkers) are performed at 1 $\mu$ M total ends concentration.

30 "Transient expression" refers to unamplified expression within about one day to two weeks of transfection. The optimal time for transient expression of a particular desired heterologous gene may vary depending on several factors including, for example, any transacting factors  
35 which may be employed, translational control mechanisms and the host cell. Transient expression occurs when the

5 particular plasmid that has been transfected functions, i.e., is transcribed and translated. During this time the plasmid DNA which has entered the cell is transferred to the nucleus. The DNA is in a nonintegrated state, free within the nucleus. Transcription of the plasmid taken up 10 by the cell occurs during this period. Following transfection the plasmid DNA may become degraded or diluted by cell division. Random integration within the cell chromatin occurs.

15 In general, vectors containing promoters and control sequences which are derived from species compatible with the host cell are used with the particular host cell. Promoters suitable for use with prokaryotic hosts 20 illustratively include the beta-lactamase and lactose promoter systems, alkaline phosphatase, the tryptophan (trp) promoter system and hybrid promoters such as tac promoter. However, other functional bacterial promoters are suitable. In addition to prokaryotes, eukaryotic microbes such as yeast cultures may also be used. 25 Saccharomyces cerevisiae, or common baker's yeast is the most commonly used eukaryotic microorganism, although a number of other strains are commonly available. Promoters controlling transcription from vectors in mammalian host 30 cells may be obtained from various sources, for example, the genomes of viruses such as: polyoma, simian virus 40 (SV40), adenovirus, retroviruses, hepatitis B virus and preferably cytomegalovirus, or from heterologous mammalian promoters, e.g.  $\beta$ -actin promoter. The early and late promoters of the SV 40 virus are conveniently obtained as 35 an SV40 restriction fragment that also contains the SV40 viral origin of replication. The immediate early promoter

5 of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment. Of course, promoters from the host cell or related species also are useful herein.

10 The vectors used herein may contain a selection gene, also termed a selectable marker. A selection gene encodes a protein, necessary for the survival or growth of a host cell transformed with the vector. Examples of suitable selectable markers for mammalian cells include the dihydrofolate reductase gene (DHFR), the ornithine 15 decarboxylase gene, the multi-drug resistance gene (mdr), the adenosine deaminase gene, and the glutamine synthase gene. When such selectable markers are successfully transferred into a mammalian host cell, the transformed mammalian host cell can survive if placed under selective 20 pressure. There are two widely used distinct categories of selective regimes. The first category is based on a cell's metabolism and the use of a mutant cell line which lacks the ability to grow independent of a supplemented media. The second category is referred to as dominant 25 selection which refers to a selection scheme used in any cell type and does not require the use of a mutant cell line. These schemes typically use a drug to arrest growth of a host cell. Those cells which have a novel gene would express a protein conveying drug resistance and would 30 survive the selection. Examples of such dominant selection use the drugs neomycin (Southern and Berg (1982) J. Molec. Appl. Genet. 1, 327), mycophenolic acid (Mulligan and Berg (1980) Science 209, 1422), or hygromycin (Sugden et al. (1985) Mol. Cell. Biol. 5, 35 410-413). The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the

5 appropriate drug neomycin (G418 or gentamicin), xgpt  
(mycophenolic acid) or hygromycin, respectively.

10 "Transfection" means introducing DNA into a host cell so  
that the DNA is expressed, whether functionally expressed  
or otherwise; the DNA may also replicate either as an  
extrachromosomal element or by chromosomal integration.  
Unless otherwise provided, the method used herein for  
transfection of the host cells is the calcium phosphate  
co-precipitation method of Graham and van der Eb (1973)  
15 Virology 52, 456-457. Alternative methods for  
transfection are electroporation, the DEAE-dextran method,  
lipofection and biolistics (Kriegler (1990) Gene Transfer  
and Expression: A Laboratory Manual, Stockton Press).

20 Host cells may be transfected with the expression vectors  
of the present invention and cultured in conventional  
nutrient media modified as is appropriate for inducing  
promoters, selecting transformants or amplifying genes.  
Host cells are cultured in F12:DMEM (Gibco) 50:50 with  
25 added glutamine. The culture conditions, such as  
temperature, pH and the like, are those previously used  
with the host cell selected for expression, and will be  
apparent to the ordinarily skilled artisan.

30 The following examples merely illustrate the best mode now  
known for practicing the invention, but should not be  
construed to limit the invention. All publications and  
patent applications cited in this specification are herein  
incorporated by reference in their entirety as if each  
35 individual publication or patent application were  
specifically and individually indicated to be incorporated

5 by reference.

**EXAMPLE 1**

**Phenotypic Drug Susceptibility and Resistance Test Using  
Resistance Test Vectors**

10 Phenotypic drug susceptibility and resistance tests are carried out using the means and methods described in US Patent Number 5,837,464 (International Publication Number WO 97/27319) which is hereby incorporated by reference.

15 In these experiments patient-derived segment(s) corresponding to the HIV protease and reverse transcriptase coding regions were either patient-derived segments amplified by the reverse transcription-polymerase chain reaction method (RT-PCR) using viral RNA isolated from viral particles present in the serum of HIV-infected 20 individuals or were mutants of wild type HIV-1 made by site directed mutagenesis of a parental clone of resistance test vector DNA. Isolation of viral RNA was performed using standard procedures (e.g. RNAgent Total 25 RNA Isolation System, Promega, Madison WI or RNAzol, Tel-Test, Friendswood, TX). The RT-PCR protocol was divided into two steps. A retroviral reverse transcriptase [e.g. Moloney MuLV reverse transcriptase (Roche Molecular Systems, Inc., Branchburg, NJ), or avian 30 myeloblastosis virus (AMV) reverse transcriptase, (Boehringer Mannheim, Indianapolis, IN)] was used to copy viral RNA into cDNA. The cDNA was then amplified using a thermostable DNA polymerase [e.g. Taq (Roche Molecular Systems, Inc., Branchburg, NJ), Tth (Roche Molecular Systems, Inc., Branchburg, NJ), PrimeZyme (isolated from 35 *Thermus brockianus*, Biometra, Gottingen, Germany)] or a

5 combination of thermostable polymerases as described for  
the performance of "long PCR" (Barnes, W.M., (1994) Proc.  
Natl. Acad. Sci, USA 91, 2216-2220) [e.g. Expand High  
Fidelity PCR System (Taq + Pwo), (Boehringer Mannheim.  
Indianapolis, IN) OR GeneAmp XL PCR kit (Tth + Vent),  
10 (Roche Molecular Systems, Inc., Branchburg, NJ)].

PCR6 (Table 5, #1) is used for reverse transcription of  
viral RNA into cDNA. The primers, ApaI primer (PDSApa,  
Table 5, #2) and AgeI primer (PDSAge, Table 5, #3) used to  
15 amplify the "test" patient-derived segments contained  
sequences resulting in ApaI and AgeI recognition sites  
being introduced into both ends of the PCR product,  
respectively.

Resistance test vectors incorporating the "test"  
20 patient-derived segments were constructed as described in  
US Patent Number 5,837,464 (International Publication  
Number WO 97/27319) (see Fig. 1) using an amplified DNA  
product of 1.5 kB prepared by RT-PCR using viral RNA as a  
template and oligonucleotides PCR6 (#1), PDSApa (#2) and  
25 PDSAge (#3) as primers, followed by digestion with ApaI  
and AgeI or the isoschizomer PinAl. To ensure that the  
plasmid DNA corresponding to the resultant resistance test  
vector comprises a representative sample of the HIV viral  
quasi-species present in the serum of a given patient,  
30 many (>100) independent E. coli transformants obtained in  
the construction of a given resistance test vector were  
pooled and used for the preparation of plasmid DNA.

A packaging expression vector encoding an amphotrophic  
35 MuLV 4070A env gene product enables production in a  
resistance test vector host cell of resistance test vector

5      viral particles which can efficiently infect human target cells. Resistance test vectors encoding all HIV genes with the exception of env were used to transfect a packaging host cell (once transfected the host cell is referred to as a resistance test vector host cell). The  
10     packaging expression vector which encodes the amphotrophic MuLV 4070A env gene product is used with the resistance test vector to enable production in the resistance test vector host cell of infectious pseudotyped resistance test vector viral particles.

15     Resistance tests performed with resistance test vectors were carried out using packaging host and target host cells consisting of the human embryonic kidney cell line 293 (Cell Culture Facility, UC San Francisco, SF, CA) or  
20     the Jurkat leukemic T-cell line (Arthur Weiss, UC San Francisco, SF, CA).

Resistance tests were carried out with resistance test vectors using two host cell types. Resistance test vector  
25     viral particles were produced by a first host cell (the resistance test vector host cell) that was prepared by transfecting a packaging host cell with the resistance test vector and the packaging expression vector. The resistance test vector viral particles were then used to  
30     infect a second host cell (the target host cell) in which the expression of the indicator gene is measured (see Fig. 2).

35     The resistance test vectors containing a functional luciferase gene cassette were constructed and host cells were transfected with the resistance test vector DNA. The

5      resistant test vectors contained patient-derived reverse transcriptase and protease DNA sequences that encode proteins which were either susceptible or resistant to the antiretroviral agents, such as nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors and protease inhibitors. The 10     resistance test vector viral particles produced by transfecting the resistance test vector DNA into host cells, either in the presence or absence of protease inhibitors, were used to infect target host cells grown 15     either in the absence of NRTI or NNRTI or in the presence of increasing concentrations of the drug. Luciferase activity in infected target host cells in the presence of drug was compared to the luciferase activity in infected target host cells in the absence of drug. Drug resistance 20     was measured as the concentration of drug required to inhibit by 50% the luciferase activity detected in the absence of drug (inhibitory concentration 50%, IC<sub>50</sub> ). The IC<sub>50</sub> values were determined by plotting percent drug inhibition vs. log<sub>10</sub> drug concentration.

25     Host cells were seeded in 10-cm-diameter dishes and were transfected one day after plating with resistance test vector plasmid DNA and the envelope expression vector. Transfections were performed using a calcium-phosphate 30     co-precipitation procedure. The cell culture media containing the DNA precipitate was replaced with fresh medium, from one to 24 hours, after transfection. Cell culture media containing resistance test vector viral particles was harvested one to four days after 35     transfection and was passed through a 0.45-mm filter before being stored at -80°C. HIV capsid protein (p24)

5 levels in the harvested cell culture media were determined by an EIA method as described by the manufacturer (SIAC; Frederick, MD). Before infection, target cells (293 and 293/T) were plated in cell culture media. Control infections were performed using cell culture media from 10 mock transfections (no DNA) or transfections containing the resistance test vector plasmid DNA without the envelope expression plasmid. One to three or more days after infection the media was removed and cell lysis buffer (Promega) was added to each well. Cell lysates 15 were assayed for luciferase activity. The inhibitory effect of the drug was determined using the following equation:

20 
$$\% \text{ luciferase inhibition} = [1 - (\text{RLULuc [drug]} / \text{RLULuc})] \times 100$$

25 where  $\text{RLULuc [drug]}$  is the relative light unit of luciferase activity in infected cells in the presence of drug and  $\text{RLULuc}$  is the Relative Light Unit of luciferase activity in infected cells in the absence of drug. IC<sub>50</sub> values were obtained from the sigmoidal curves that were generated from the data by plotting the percent inhibition of luciferase activity vs. the log<sub>10</sub> drug concentration. Examples of drug inhibition curves are shown in (Fig. 3).

30

#### EXAMPLE 2

**An in vitro Assay Using Resistance Test Vectors And Site Directed Mutants To Correlate Phenotypes And Genotypes Associated With HIV Drug Susceptibility And Resistance**

35 Phenotypic susceptibility analysis of patient HIV samples Resistance test vectors are constructed as described in

5 example 1. Resistance test vectors, or clones derived from  
the resistance test vector pools, are tested in a  
phenotypic assay to determine accurately and  
quantitatively the level of susceptibility to a panel of  
anti-retroviral drugs. This panel of anti-retroviral  
10 drugs may comprise members of the classes known as  
nucleoside-analog reverse transcriptase inhibitors  
(NRTIs), non-nucleoside reverse transcriptase inhibitors  
(NNRTIs), and protease inhibitors (PRIs). The panel of  
drugs can be expanded as new drugs or new drug targets  
15 become available. An IC<sub>50</sub> is determined for each  
resistance test vector pool for each drug tested. The  
pattern of susceptibility to all of the drugs tested is  
examined and compared to known patterns of susceptibility.

20 A patient sample can be further examined for genotypic  
changes correlated with the pattern of susceptibility  
observed.

**Genotypic analysis of patient HIV samples**

Resistance test vector DNAs, either pools or clones, are  
25 analyzed by any of the genotyping methods described in  
Example 1. In one embodiment of the invention, patient  
HIV sample sequences are determined using viral RNA  
purification, RT/PCR and ABI chain terminator automated  
sequencing. The sequence that is determined is compared  
30 to control sequences present in the database or is  
compared to a sample from the patient prior to initiation  
of therapy, if available. The genotype is examined for  
sequences that are different from the control or  
pre-treatment sequence and correlated to the observed  
35 phenotype.

5      **Phenotypic susceptibility analysis of site directed mutants**

Genotypic changes that are observed to correlate with changes in phenotypic patterns of drug susceptibility are evaluated by construction of resistance test vectors 10 containing the specific mutation on a defined, wild-type (drug susceptible) genetic background. Mutations may be incorporated alone and/or in combination with other mutations that are thought to modulate the susceptibility of HIV to a certain drug or class of drugs. Mutations are 15 introduced into the resistance test vector through any of the widely known methods for site-directed mutagenesis. In one embodiment of this invention the mega-primer PCR method for site-directed mutagenesis is used. A resistance test vector containing the specific mutation or 20 group of mutations are then tested using the phenotypic susceptibility assay described above and the susceptibility profile is compared to that of a genetically defined wild-type (drug susceptible) resistance test vector which lacks the specific mutations. 25 Observed changes in the pattern of phenotypic susceptibility to the antiretroviral drugs tested are attributed to the specific mutations introduced into the resistance test vector.

30      **EXAMPLE 3**

Using Resistance Test Vectors To Correlate Genotypes And Phenotypes Associated With Changes in PRI Drug Susceptibility in HIV.

**Phenotypic analysis of Patient 0732**

35      A resistance test vector was constructed as described in example 1 from a patient sample designated as 0732. This

5 patient had been previously treated with nelfinavir. Isolation of viral RNA and RT/PCR was used to generate a patient derived segment that comprised viral sequences coding for all of PR and aa 1 - 313 of RT. The patient derived segment was inserted into an indicator gene viral 10 vector to generate a resistance test vector designated RTV-0732. RTV-0732 was tested using a phenotypic susceptibility assay to determine accurately and quantitatively the level of susceptibility to a panel of anti-retroviral drugs. This panel of anti-retroviral 15 drugs comprised members of the classes known as NRTIs (AZT, 3TC, d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine, nevirapine and efavirenz), and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and amprenavir). An IC<sub>50</sub> was determined for each drug tested. 20 Susceptibility of the patient virus to each drug was examined and compared to known patterns of susceptibility. A pattern of susceptibility to the PRIs was observed for patient sample RTV-0732 in which there was a decrease in both nelfinavir and indinavir susceptibility (increased 25 resistance) and an increase in amprenavir susceptibility (see Fig. 4 and Table 1). Patient sample 0732 was examined further for genotypic changes associated with the pattern of susceptibility.

30 **Determination of genotype of patient 0732**

RTV-0732 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The 35 nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were

5 noted at positions K14R, I15V, K20T, E35D, M36I, R41K,  
I62V, L63Q and N88S. K14R, I15V, E35D, R41K and I62V are  
naturally occurring polymorphisms in HIV-1 PR and are not  
associated with reduced susceptibility to any drug. M36I  
has previously been described to be associated with  
10 resistance to ritonavir and nelfinavir (Shihazi, 1998).  
N88S has previously been described to be associated with  
resistance to nelfinavir (Patock AAC, 42: 2637 (1998) and  
an investigational PRI, SC55389A (Smidt, 1997).

15 **Phenotypic analysis of Patient 627**

A resistance test vector was constructed as described in  
example 1 from a patient sample designated as 627. This  
patient had been treated with indinavir. Isolation of  
viral RNA and RT/PCR was used to generate a patient  
20 derived segment that comprised viral sequences coding for  
all of PR and aa 1 - 313 of RT. The patient derived  
segment was inserted into an indicator gene viral vector  
to generate a resistance test vector designated RTV-627.  
RTV-627 was tested using a phenotypic susceptibility assay  
25 to determine accurately and quantitatively the level of  
susceptibility to a panel of anti-retroviral drugs. This  
panel of anti-retroviral drugs comprised members of the  
classes known as NRTIs (AZT, 3TC, d4T, ddI, ddC, and  
abacavir), NNRTIs (delavirdine, nevirapine and efavirenz),  
30 and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and  
amprenavir). An IC50 was determined for each drug tested.  
Susceptibility of the patient virus to each drug was  
examined and compared to known patterns of susceptibility.  
A pattern of susceptibility to the PRIs was observed for  
35 patient sample RTV-627 in which there was a decrease in  
indinavir and nelfinavir susceptibility (increased

5 resistance) and an increase in amprenavir and saquinavir susceptibility. Patient sample 627 was examined further for genotypic changes associated with the pattern of susceptibility.

10 **Determination of genotype of patient 627**

RTV-627 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were noted at positions I31V, E35D, M46L, L63P, I64V, I73V and N88S. I13V, E35D and I64V are naturally occurring polymorphisms in HIV-1 PR and are not associated with reduced susceptibility to any drug. M46L has previously been described to be associated with resistance to indinavir and amprenavir. L63P has previously been described to be associated with resistance to indinavir and nelfinavir. N88S has previously been described to be associated with resistance to nelfinavir (Patick, 1998) and an investigational PRI, SC55389A (Smidt, 1997).

**Phenotypic analysis of Patient 1208**

30 A resistance test vector was constructed as described in example 1 from a patient sample designated as 1208. This patient had been previously treated with nelfinavir. Isolation of viral RNA and RT/PCR was used to generate a patient derived segment that comprised viral sequences coding for all of PR and aa 1 - 313 of RT. The patient 35 derived segment was inserted into an indicator gene viral vector to generate a resistance test vector designated

5 RTV-1208. RTV-1208 was tested using a phenotypic  
susceptibility assay to determine accurately and  
quantitatively the level of susceptibility to a panel of  
anti-retroviral drugs. This panel of anti-retroviral drugs  
comprised members of the classes known as NRTIs (AZT, 3TC,  
10 d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine,  
nevirapine and efavirenz), and PRIs (indinavir,  
nelfinavir, ritonavir, saquinavir and amprenavir). An IC<sub>50</sub>  
was determined for each drug tested. Susceptibility of  
the patient virus to each drug was examined and compared  
15 to known patterns of susceptibility. A pattern of  
susceptibility to the PRIs was observed for patient sample  
RTV-1208 in which there was a decrease in indinavir and  
nelfinavir susceptibility (increased resistance) and an  
increase in amprenavir susceptibility. Patient sample  
20 1208 was examined further for genotypic changes associated  
with the pattern of susceptibility.

**Determination of genotype of patient 1208**

RTV-1208 DNA was analyzed by ABI chain terminator  
25 automated sequencing. The nucleotide sequence was  
compared to the consensus sequence of a wild type clade B  
HIV-1 (HIV Sequence Database Los Alamos, NM). The  
nucleotide sequence was examined for sequences that are  
30 different from the control sequence. PR mutations were  
noted at positions I62V, L63P, V77I, and N88S. I62V is a  
naturally occurring polymorphism in HIV-1 PR and is not  
associated with reduced susceptibility to any drug. L63P  
has previously been described to be associated with  
resistance to indinavir and nelfinavir. V77I has  
35 previously been described to be associated with resistance  
to nelfinavir. N88S has previously been described to be

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5      associated with resistance to nelfinavir (Patick, 1998)  
and an investigational PRI, SC55389A (Smidt, 1997).

10     **Phenotypic analysis of Patient 360**

A resistance test vector was constructed as described in example 1 from a patient sample designated as 360. This patient had been previously treated with indinavir. Isolation of viral RNA and RT/PCR was used to generate a patient derived segment that comprised viral sequences coding for all of PR and aa 1 - 313 of RT. The patient derived segment was inserted into an indicator gene viral vector to generate a resistance test vector designated RTV-360. RTV-360 was tested using a phenotypic susceptibility assay to determine accurately and quantitatively the level of susceptibility to a panel of anti-retroviral drugs. This panel of anti-retroviral drugs comprised members of the classes known as NRTIs (AZT, 3TC, d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine, nevirapine and efavirenz), and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and amprenavir). An IC<sub>50</sub> was determined for each drug tested. Susceptibility of the patient virus to each drug was examined and compared to known patterns of susceptibility. A pattern of susceptibility to the PRIs was observed for patient sample RTV-360 in which there was a decrease in indinavir and nelfinavir susceptibility (increased resistance) and an increase in amprenavir susceptibility. Patient sample 360 was examined further for genotypic changes associated with the pattern of susceptibility.

5      **Determination of genotype of patient 360**

RTV-360 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were noted at positions I13V, K20M, M36V, N37A, M46I, I62V, L63P, N88S, and I93L. I13V, N37A and I62V are naturally occurring polymorphisms in HIV-1 PR and are not associated with reduced susceptibility to any drug. K20M has previously been described to be associated with resistance to indinavir. M46I has previously been described to be associated with resistance to indinavir, ritonavir, nelfinavir and amprenavir. L63P has previously been described to be associated with resistance to indinavir and nelfinavir. N88S has previously been described to be associated with resistance to nelfinavir (Patick, 1998) and an investigational PRI, SC55389A (Smidt, 1997).

25      **Phenotypic analysis of Patient 0910**

A resistance test vector was constructed as described in example 1 from a patient sample designated as 0910. This patient had been previously treated with nelfinavir. Isolation of viral RNA and RT/PCR was used to generate a patient derived segment that comprised viral sequences coding for all of PR and aa 1 - 313 of RT. The patient derived segment was inserted into an indicator gene viral vector to generate a resistance test vector designated RTV-0910. RTV-0910 was tested using a phenotypic susceptibility assay to determine accurately and quantitatively the level of susceptibility to a panel of

5 anti-retroviral drugs. This panel of anti-retroviral drugs comprised members of the classes known as NRTIs (AZT, 3TC, d4T, dDI, ddC, and abacavir), NNRTIs (delavirdine, nevirapine and efavirenz), and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and amprenavir). An IC50 was determined for each drug tested. Susceptibility of the patient virus to each drug was examined and compared to known patterns of susceptibility. A pattern of susceptibility to the PRIs was observed for patient sample RTV-0910 in which there was a decrease in indinavir and 10 nelfinavir susceptibility (increased resistance) and an increase in amprenavir susceptibility. Patient sample 15 0910 was examined further for genotypic changes associated with the pattern of susceptibility.

20 **Determination of genotype of patient 0910**

RTV-0910 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The 25 nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were noted at positions M46I, L63P, V77I, N88S and I93I/L. I13V, K14R, N37D and I193L are naturally occurring polymorphism in HIV-1 PR and is not associated with 30 reduced susceptibility to any drug. V77I has previously been described to be associated with resistance to nelfinavir. M46I has previously been described to be associated with resistance to indinavir, ritonavir, nelfinavir and amprenavir. L63P has previously been 35 described to be associated with resistance to indinavir and nelfinavir. N88S has previously been described to be

5      associated with resistance to nelfinavir (Patick, 1998)  
and an investigational PRI, SC55389A (Smidt, 1997).

**Phenotypic analysis of Patient 3542**

A resistance test vector was constructed as described in  
10     example 1 from a patient sample designated as 3542. This  
patient had been treated with indinavir. Isolation of  
viral RNA and RT/PCR was used to generate a patient  
derived segment that comprised viral sequences coding for  
all of PR and aa 1 - 313 of RT. The patient derived  
15     segment was inserted into an indicator gene viral vector  
to generate a resistance test vector designated RTV-3542.  
RTV-3542 was tested using a phenotypic susceptibility  
assay to determine accurately and quantitatively the level  
of susceptibility to a panel of anti-retroviral drugs.  
20     This panel of anti-retroviral drugs comprised members of  
the classes known as NRTIs (AZT, 3TC, d4T, ddI, ddC, and  
abacavir), NNRTIs (delavirdine, nevirapine and efavirenz),  
and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and  
amprenavir). An IC50 was determined for each drug tested.  
25     Susceptibility of the patient virus to each drug was  
examined and compared to known patterns of susceptibility.  
A pattern of susceptibility to the PRIs was observed for  
patient sample RTV-3542 in which there was a decrease in  
indinavir, nelfinavir and ritonavir susceptibility  
30     (increased resistance) and an increase in amprenavir  
susceptibility. Patient sample 3542 was examined further  
for genotypic changes associated with the pattern of  
susceptibility.

35     Determination of genotype of patient 3542  
RTV-3542 DNA was analyzed by ABI chain terminator

5 automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B HIV-1 (HIV Sequence Database Los Alamos, NM). The nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were  
10 noted at positions I13V, K14R, N37D, M46I, L63P, N88S and I93L. K14R and N37A/D are naturally occurring polymorphisms in HIV-1 PR and are not associated with reduced susceptibility to any drug. M46I has previously been described to be associated with resistance to  
15 indinavir, ritonavir, nelfinavir and amprenavir. L63P has previously been described to be associated with resistance to indinavir and nelfinavir. N88S has previously been described to be associated with resistance to nelfinavir (Patock, 1998) and an investigational PRI, SC55389A  
20 (Smidt, 1997).

**Phenotypic analysis of Patient 3654**

A resistance test vector was constructed as described in example 1 from a patient sample designated as 3654. This  
25 patient had been previously treated with ritonavir. Isolation of viral RNA and RT/PCR was used to generate a patient derived segment that comprised viral sequences coding for all of PR and aa 1 - 313 of RT. The patient derived segment was inserted into an indicator gene viral  
30 vector to generate a resistance test vector designated RTV-3654. RTV-3654 was tested using a phenotypic susceptibility assay to determine accurately and quantitatively the level of susceptibility to a panel of anti-retroviral drugs. This panel of anti-retroviral drugs  
35 comprised members of the classes known as NRTIs (AZT, 3TC, d4T, ddI, ddC, and abacavir), NNRTIs (delavirdine,

5 nevirapine and efavirenz), and PRIs (indinavir, nelfinavir, ritonavir, saquinavir and amprenavir). An IC50 was determined for each drug tested. Susceptibility of the patient virus to each drug was examined and compared to known patterns of susceptibility. A pattern of 10 susceptibility to the PRIs was observed for patient sample RTV-3654 in which there was a decrease in indinavir and nelfinavir susceptibility (increased resistance) and an increase in amprenavir susceptibility. Patient sample 3654 was examined further for genotypic changes associated 15 with the pattern of susceptibility.

**Determination of genotype of patient 3654**

RTV-3654 DNA was analyzed by ABI chain terminator automated sequencing. The nucleotide sequence was compared to the consensus sequence of a wild type clade B 20 HIV-1 (HIV Sequence Database Los Alamos, NM). The nucleotide sequence was examined for sequences that are different from the control sequence. PR mutations were noted at positions I13V, R41K, M46I, L63P, V77I, N88S and 25 I93L. I13V, R41K and I93L are naturally occurring polymorphism in HIV-1 PR and is not associated with reduced susceptibility to any drug. M46I has previously been described to be associated with resistance to indinavir, ritonavir, nelfinavir and amprenavir. L63P has 30 previously been described to be associated with resistance to indinavir and nelfinavir. V77I has previously been described to be associated with resistance to nelfinavir. N88S has previously been described to be associated with resistance to an investigational PRI, SC55389A (Smidt, 35 1997).

5

**EXAMPLE 4****Using Site Directed Mutants To Correlate Genotypes And Phenotypes Associated With Changes in PR1 Drug Susceptibility in HIV.****Site directed mutagenesis**

10 Resistance test vectors were constructed containing the N88S mutation alone and in combination with other substitutions in PR (L63P, V77I and M46L) known to modulate the HIV susceptibility to PRIs. Mutations were introduced into the resistance test vector using the  
15 mega-primer PCR method for site-directed mutagenesis. (Sakar G and Sommar SS (1994) Biotechniques 8(4), 404-407). First, a resistance test vector was constructed that harbors a unique RsrII restriction site 590 bp downstream of the ApaI restriction site. The 590 bp ApaI - RsrII fragment thus contains the entire protease region.  
20 This site was introduced by site-specific oligonucleotide-directed mutagenesis using primer #4. All subsequent mutants were constructed by fragment-exchange of the wild-type ApaI - RsrII fragment in the parent vector with the equivalent fragment carrying the  
25 respective mutations.

A resistance test vector containing the N88S mutation (N88S-RTV) was tested using the phenotypic susceptibility assay described above and the results were compared to that of a genetically defined resistance test vector that was wild type at position 88. The pattern of phenotypic susceptibility to the PRIs in the N88S-RTV was altered as compared to wild type. In the context of an otherwise wild type background (i.e. N88S mutation alone) the N88S-RTV was more susceptible to both amprenavir and

5 ritonavir and slightly less susceptible to nelfinavir compared to the wild type control RTV (see Table 2).

A resistance test vector containing the N88S mutation along with the L63P mutation (L63P-N88S-RTV) was tested  
10 using the phenotypic susceptibility assay described above and the results were compared to that of a genetically defined resistance test vector that was wild type at positions 63 and 88. The L63P-N88S-RTV showed decreased susceptibility to both indinavir and nelfinavir and an  
15 increase in the susceptibility to amprenavir compared the wild-type control RTV (see Table 2). Thus it appears that the introduction of a second mutation, L63P, in addition to N88S, results in a reduction in susceptibility to nelfinavir and indinavir while the increased  
20 susceptibility to amprenavir is maintained.

A resistance test vector containing the N88S mutation along with the L63P mutation and the V77I mutation (L63P-V77I-N88S-RTV) was tested using the phenotypic susceptibility assay described above and the results were compared to that of a genetically defined resistance test vector that was wild type at positions 63 and 77 and 88. The RTV containing mutations at these positions, L63P-V77I-N88S-RTV, showed a decrease in susceptibility to both indinavir and nelfinavir and an increase in the susceptibility to amprenavir compared to the wild-type control RTV (see Fig. 5 and Table 2). Thus it appears that the introduction of a third mutation, V77I, in addition to L63P and N88S, results in a reduction in susceptibility to nelfinavir and indinavir while the increased susceptibility to amprenavir is maintained.  
30  
35

5

The N88S mutation was also introduced into an RTV containing additional mutations at positions L63P and M46L (M46L + L63P + N88S). The RTV containing mutations at these positions, M46L-L63P-N88S-RTV showed a decrease in 10 susceptibility to nelfinavir and a slight decrease in the susceptibility to indinavir and an increase in the susceptibility to amprenavir compared to the wild-type control RTV (see Fig. 5 and Table 2). Thus it appears that the introduction of a third mutation, M46L, in 15 addition to L63P and N88S, results in a reduction in susceptibility to nelfinavir and indinavir while the increased susceptibility to amprenavir is maintained.

A resistance test vector containing the N88S mutation 20 along with the M46L mutation, the L63P mutation, and the V77I mutation (M46L-L63P-V77I-N88S-RTV) was tested using the phenotypic susceptibility assay described above and the results were compared to that of a genetically defined resistance test vector that was wild type at positions 46, 25 63, 77 and 88. The RTV containing mutations at these four positions, M46L-L63P-V77I-N88S-RTV showed a decrease in susceptibility to nelfinavir and indinavir and an increase in the susceptibility to amprenavir compared to the wild-type control RTV (see Fig. 5 and Table 2). Thus it 30 appears that the introduction of a fourth mutation, V77I, in addition to L63P, M46L and N88S results in a reduction in susceptibility to nelfinavir and indinavir while the increased susceptibility to amprenavir is maintained. A resistance test vector containing the L63P mutation 35 (L63P-RTV) was tested using the phenotypic susceptibility assay described above and the results were compared to

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5 that of a genetically defined resistance test vector that was wild type at position 63. The pattern of phenotypic susceptibility to the PRIs in the L63P-RTV was similar to wild type with no significant changes in susceptibility to the PRIs observed.

10 The L63P mutation was also introduced into an RTV containing an additional mutation at position V77I. The L63P-V77I-RTV showed a slight decrease in susceptibility to nelfinavir compared to the wild-type control RTV (see 15 Fig. 5 and Table 2).

#### EXAMPLE 5

##### **Predicting Response to Protease Inhibitors by Characterization of Amino Acid 88 of HIV-1 Protease.**

20 In one embodiment of this invention, changes in the amino acid at position 88 of the protease protein of HIV-1 is evaluated using the following method comprising: (i) collecting a biological sample from an HIV-1 infected 25 subject; (ii) evaluating whether the biological sample contains nucleic acid encoding HIV-1 protease having an asparagine to serine mutation at codon 88 (N88S); and (iii) determining susceptibility to protease inhibitors (PRI).

30 The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, 35 cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid

5 (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after purification of virus particles from the biological sample. Evaluating whether the amino acid at position 88 of the HIV-1 protease is mutated to serine, can be performed using various methods, such as direct characterization of the viral nucleic acid encoding protease or direct characterization of the protease protein itself. Defining the amino acid at position 88 of protease can be performed by direct characterization of 10 the protease protein by conventional or novel amino acid sequencing methodologies, epitope recognition by antibodies or other specific binding proteins or compounds. Alternatively, the amino acid at position 88 of the HIV-1 protease protein can be defined by 15 characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 nucleic acid can be performed using a variety of methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The 20 nucleic acid sequence encoding HIV protease at codon 88 can be determined by direct nucleic acid sequencing using various primer extension-chain termination (Sanger, ABI/PE and Visible Genetics) or chain cleavage (Maxam and Gilbert) methodologies or more recently developed 25 sequencing methods such as matrix assisted laser desorption-ionization time of flight (MALDI-TOF) or mass spectrometry (Sequenom, Gene Trace Systems). Alternatively, the nucleic acid sequence encoding amino acid position 88 can be evaluated using a variety of probe 30 hybridization methodologies, such as genechip hybridization sequencing (Affymetrix), line probe assay 35

5 (LiPA; Murex), and differential hybridization (Chiron).

In a preferred embodiment of this invention, evaluation of protease inhibitor susceptibility and of whether amino acid position 88 of HIV-1 protease was wild type or serine 10 was carried out using a phenotypic susceptibility assay or genotypic assay, respectively, using resistance test vector DNA prepared from the biological sample. In one embodiment, the plasma sample was collected, viral RNA was purified and an RT-PCR methodology was used to amplify a 15 patient derived segment encoding the HIV-1 protease and reverse transcriptase regions. The amplified patient derived segments were then incorporated, via DNA ligation and bacterial transformation, into an indicator gene viral vector thereby generating a resistance test vector. 20 Resistance test vector DNA was isolated from the bacterial culture and the phenotypic susceptibility assay was carried out as described in Example 1. The results of the phenotypic susceptibility assay with a patient sample having an N88S mutation in PR is shown in Figure 4. The 25 nucleic acid (DNA) sequence of the patient derived HIV-1 protease and reverse transcriptase regions from patient sample 0732 was determined using a fluorescence detection chain termination cycle sequencing methodology (ABI/PE). The method was used to determine a consensus nucleic acid 30 sequence representing the combination of sequences of the mixture of HIV-1 variants existing in the subject sample (representing the quasispecies), and to determine the nucleic acid sequences of individual variants.

35 **Phenotypic and genotypic correlation of mutations at amino acid 88 of HIV-1 Protease.**

5      Phenotypic susceptibility profiles of patient samples and  
site directed mutants showed that amprenavir  
susceptibility correlated with the presence of the N88S  
mutation in HIV-1 protease. Phenotypic susceptibility  
profiles of patient samples and site directed mutants  
10     showed that a significant increase in amprenavir  
susceptibility (decreased resistance) correlated with a  
mutation in the nucleic acid sequence encoding the amino  
acid serine (S) at position 88 of HIV-1 protease.

15     Phenotypic susceptibility profiles of patient samples and  
site directed mutants showed reduction in amprenavir  
susceptibility (decreased resistance) and a decrease in  
susceptibility to nelfinavir and indinavir with the amino  
acid serine at position 88 when the PR mutations at  
20     positions 63, 77 or 46 were also present (L63P, V77I, or  
M46L).

#### EXAMPLE 6

25     **Using Resistance test vectors and site directed mutants to  
correlate genotypes associated with alterations in PR  
susceptibility with viral fitness.**

30     Luciferase activity measured in the absence of drug for  
the seven resistance test vectors constructed from the  
patient viruses containing the N88S PR mutation ranged  
from 0.7 to 16% of control (Table 3). Although these  
viruses also contain multiple mutations in reverse  
transcriptase, which could also contribute to a reduction  
35     in viral fitness, the data suggest that viruses containing  
the N88S mutation are less fit than wild type. To confirm

5 this observation, the luciferase expression level for the site-directed mutant resistance test vectors was also examined.

10 Viruses containing N88S as the only substitution produced only 1.0% of the luciferase activity in the absence of drug (Table 4). This reduction was substantially alleviated by the addition of the L63P substitution (20.7%) or by addition of the combinations of L63P/V77I (29.3%) or M46L/L63P (28.0%). The L63P or L63P/V77I 15 mutants had equivalent or increased relative luciferase activity compared to wild type (163.9 and 75.6%, respectively).

20 When the K20T substitution was added to the N88S background, either alone or in combination with L63P, only background levels of luciferase activity was detected. Sequence analysis confirmed the absence of additional mutations, which might render the vector inactive. Thus 25 the combination of the K20T and N88S substitutions correlates with a severe defect in fitness.

#### EXAMPLE 7

30 **Predicting Response to Protease Inhibitors by Characterization of Amino Acid 82 of HIV-1 Protease.**

In one embodiment of this invention, changes in the amino acid at position 82 of the protease protein of HIV-1 are evaluated using the following method comprising: (i) 35 collecting a biological sample from an HIV-1 infected subject; (ii) evaluating whether the biological sample

5 contains nucleic acid encoding HIV-1 protease having a valine to alanine (V82A), phenylalanine (V82F), serine (V82S), or threonine (V82T) substitution at codon 82; and (iii) determining susceptibility to protease inhibitors (PRI).

10 The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, 15 cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after purification of virus particles from the biological 20 sample. Evaluating whether the amino acid at position 82 of the HIV-1 protease is mutated to alanine, phenylalanine, serine, or threonine, can be performed using various methods, such as direct characterization of the viral nucleic acid encoding protease or direct 25 characterization of the protease protein itself. Defining the amino acid at position 82 of protease can be performed by direct characterization of the protease protein by conventional or novel amino acid sequencing methodologies, epitope recognition by antibodies or other specific 30 binding proteins or compounds. Alternatively, the amino acid at position 82 of the HIV-1 protease protein can be defined by characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 nucleic acid can be performed using a variety 35 of methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA,

5 SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV  
protease at codon 82 can be determined by direct nucleic  
acid sequencing using various primer extension-chain  
termination (Sanger, ABI/PE and Visible Genetics) or chain  
cleavage (Maxam and Gilbert) methodologies or more  
10 recently developed sequencing methods such as matrix  
assisted laser desorption-ionization time of flight  
(MALDI-TOF) or mass spectrometry (Sequenom, Gene Trace  
Systems). Alternatively, the nucleic acid sequence  
encoding amino acid position 82 can be evaluated using a  
15 variety of probe hybridization methodologies, such as  
genechip hybridization sequencing (Affymetrix), line probe  
assay (LiPA; Murex), and differential hybridization  
(Chiron).

20 In a preferred embodiment of this invention, evaluation of  
protease inhibitor susceptibility and of whether amino  
acid position 82 of HIV-1 protease was wild type or  
alanine, phenylalanine, serine, or threonine, was carried  
25 out using a phenotypic susceptibility assay or genotypic  
assay, respectively, using resistance test vector DNA  
prepared from the biological sample. In one embodiment,  
the plasma sample was collected, viral RNA was purified  
and an RT-PCR methodology was used to amplify a patient  
derived segment encoding the HIV-1 protease and reverse  
30 transcriptase regions. The amplified patient derived  
segments were then incorporated, via DNA ligation and  
bacterial transformation, into an indicator gene viral  
vector thereby generating a resistance test vector.  
Resistance test vector DNA was isolated from the bacterial  
35 culture and the phenotypic susceptibility assay was  
carried out and analyzed as described in Example 1.

5

The nucleic acid (DNA) sequence of the patient derived HIV-1 protease and reverse transcriptase regions was determined using a fluorescence detection chain termination cycle sequencing methodology (ABI/PE). The 10 method was used to determine a consensus nucleic acid sequence representing the combination of sequences of the mixture of HIV-1 variants existing in the subject sample (representing the quasispecies), and to determine the nucleic acid sequences of individual variants. Genotypes 15 are analyzed as lists of amino acid differences between virus in the patient sample and a reference laboratory strain of HIV-1, NL4-3. Genotypes and corresponding phenotypes (fold-change in IC50 values) are entered in a relational database linking these two results with patient 20 information. Large datasets can then be assembled from patient virus samples sharing particular characteristics, such as the presence of any given mutation, or combination of mutations or reduced susceptibility to any drug or combination of drugs.

25

**(a) Protease inhibitor susceptibility of viruses containing mutations at amino acid 82 of HIV-1 Protease.**

Phenotypic susceptibility profiles of 75 patient virus 30 samples which contained a mutation at position 82 (V82A, F, S, or T), but no other primary mutations, were analyzed. According to most published guidelines, such viruses are expected to be resistant to ritonavir, nelfinavir, indinavir, and saquinavir. However, 8%, 20%, 35 23%, and 73% of these samples were phenotypically susceptible to these four protease inhibitors,

5 respectively (see Table 6). Thus, particularly for indinavir and saquinavir, there was poor correlation between the presence of mutations at position 82 and drug susceptibility.

10 **(b) Indinavir susceptibility of viruses containing combinations of mutations at amino acid 82 and one secondary mutation in HIV-1 Protease.**

15 Indinavir resistance in viruses containing mutations at position 82 was evaluated with respect to the presence of other specific mutations. Decreased indinavir susceptibility (fold-change in IC<sub>50</sub> greater than 2.5) in viruses containing V82A, F, S, or T but no other primary mutations was correlated with the presence of mutations at secondary positions. Reduced indinavir susceptibility was 20 observed in 20 samples containing mutations at both positions 24 and 82 (100%) and in 27 samples with both 71 and 82 (100%) (See Table 7). The combination of mutations at position 82 with mutations at other positions (e.g. 54, 46, 10, and 63) also significantly increased the 25 proportion of samples that had reduced indinavir susceptibility (Table 7).

30 **(c) Saquinavir susceptibility of viruses containing combinations of mutations at amino acid 82 and one secondary mutation in HIV-1 Protease.**

Saquinavir resistance in viruses containing mutations at position 82 was evaluated with respect to the presence of other specific mutations. Decreased saquinavir susceptibility (fold-change in IC<sub>50</sub> greater than 2.5) in 35 viruses containing V82A, F, S, or T but no other primary mutations was correlated with the presence of mutations at

5 secondary positions. Reduced saquinavir susceptibility was observed in 4 of 5 samples containing mutations at both positions 20 and 82 (80%) and in 8 of 11 samples with both 10 36 and 82 (73%) (See Table 8). The combination of mutations at position 82 with mutations at other positions (e.g. 24, 71, 54, and 10) also significantly increased the proportion of samples that had reduced saquinavir 15 susceptibility (Table 8).

(d) *Indinavir susceptibility of viruses containing combinations of mutations at amino acid 82 and many secondary mutations in HIV-1 Protease.*

Indinavir resistance in viruses containing mutations at position 82 was evaluated with respect to the presence of a defined number of other mutations. Decreased indinavir 20 susceptibility (fold-change in IC<sub>50</sub> greater than 2.5) in viruses containing V82A, F, S, or T but no other primary mutations was correlated with the number of mutations at secondary positions. Reduced indinavir susceptibility was observed in 100% of samples with V82A, F, S, or T and at 25 least 6 other secondary mutations (See Table 9). The proportion of samples that had reduced indinavir susceptibility increased significantly in samples with V82A, F, S, or T combined with 3 to 5 other secondary mutations (Table 9).

30 (e) *Saquinavir susceptibility of viruses containing combinations of mutations at amino acid 82 and many secondary mutations in HIV-1 Protease.*

Saquinavir resistance in viruses containing mutations at 35 position 82 was evaluated with respect to the presence of a defined number of other mutations. Decreased saquinavir

5      susceptibility (fold-change in IC<sub>50</sub> greater than 2.5) in viruses containing V82A, F, S, or T but no other primary mutations was correlated with the number of mutations at secondary positions. Reduced saquinavir susceptibility was observed in 60 to 76% of samples with V82A, F, S, or T  
10     and at least 5 other secondary mutations (See Table 9). The proportion of samples that had reduced saquinavir susceptibility increased significantly in samples with V82A, F, S, or T combined with 3 or 4 other secondary mutations (Table 9).

15

**EXAMPLE 8****Predicting Response to Protease Inhibitors by Characterization of Amino Acid 90 of HIV-1 Protease.**

20

In one embodiment of this invention, changes in the amino acid at position 90 of the protease protein of HIV-1 are evaluated using the following method comprising: (i) collecting a biological sample from an HIV-1 infected  
25     subject; (ii) evaluating whether the biological sample contains nucleic acid encoding HIV-1 protease having a leucine to methionine (L90M) substitution at codon 90; and (iii) determining susceptibility to protease inhibitors (PRI).

30

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, 35     cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid

5 (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after purification of virus particles from the biological sample. Evaluating whether the amino acid at position 90 of the HIV-1 protease is mutated to methionine, can be 10 performed using various methods, such as direct characterization of the viral nucleic acid encoding protease or direct characterization of the protease protein itself. Defining the amino acid at position 90 of protease can be performed by direct characterization of 15 the protease protein by conventional or novel amino acid sequencing methodologies, epitope recognition by antibodies or other specific binding proteins or compounds. Alternatively, the amino acid at position 90 of the HIV-1 protease protein can be defined by 20 characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 nucleic acid can be performed using a variety of methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The 25 nucleic acid sequence encoding HIV protease at codon 90 can be determined by direct nucleic acid sequencing using various primer extension-chain termination (Sanger, ABI/PE and Visible Genetics) or chain cleavage (Maxam and Gilbert) methodologies or more recently developed 30 sequencing methods such as matrix assisted laser desorption-ionization time of flight (MALDI-TOF) or mass spectrometry (Sequenom, Gene Trace Systems). Alternatively, the nucleic acid sequence encoding amino acid position 90 can be evaluated using a variety of probe 35 hybridization methodologies, such as genechip hybridization sequencing (Affymetrix), line probe assay

5 (LiPA; Murex), and differential hybridization (Chiron).

In a preferred embodiment of this invention, evaluation of protease inhibitor susceptibility and of whether amino acid position 90 of HIV-1 protease was wild type or 10 methionine, was carried out using a phenotypic susceptibility assay or genotypic assay, respectively, using resistance test vector DNA prepared from the biological sample. In one embodiment, the plasma sample was collected, viral RNA was purified and an RT-PCR 15 methodology was used to amplify a patient derived segment encoding the HIV-1 protease and reverse transcriptase regions. The amplified patient derived segments were then incorporated, via DNA ligation and bacterial transformation, into an indicator gene viral vector 20 thereby generating a resistance test vector. Resistance test vector DNA was isolated from the bacterial culture and the phenotypic susceptibility assay was carried out and analyzed as described in Example 1.

25 The nucleic acid (DNA) sequence of the patient derived HIV-1 protease and reverse transcriptase regions was determined using a fluorescence detection chain 30 termination cycle sequencing methodology (ABI/PE). The method was used to determine a consensus nucleic acid sequence representing the combination of sequences of the mixture of HIV-1 variants existing in the subject sample (representing the quasispecies), and to determine the nucleic acid sequences of individual variants. Genotypes are analyzed as lists of amino acid differences between 35 virus in the patient sample and a reference laboratory strain of HIV-1, NL4-3. Genotypes and corresponding

5 phenotypes (fold-change in IC<sub>50</sub> values) are entered in a relational database linking these two results with patient information. Large datasets can then be assembled from patient virus samples sharing particular characteristics, such as the presence of any given mutation, or combination 10 of mutants, or reduced susceptibility to any drug or combination of drugs.

***(a) Protease inhibitor susceptibility of viruses containing mutations at amino acid 90 of HIV-1 Protease.***

15 Phenotypic susceptibility profiles of 58 patient virus samples which contained a mutation at position 90 (L90M), but no other primary mutations, were analyzed. According to most published guidelines, such viruses are expected to 20 be resistant to ritonavir, nelfinavir, indinavir, and saquinavir. However, 28%, 9%, 31%, and 47% of these samples were phenotypically susceptible to these four protease inhibitors, respectively (see Table 6). Thus, particularly for indinavir and saquinavir, there was poor 25 correlation between the presence of mutations at position 90 and drug susceptibility.

***(b) Indinavir susceptibility of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.***

30 Indinavir resistance in viruses containing mutations at position 90 was evaluated with respect to the presence of other specific mutations. Decreased indinavir 35 susceptibility (fold-change in IC<sub>50</sub> greater than 2.5) in viruses containing L90M but no other primary mutations was correlated with the presence of mutations at secondary

5 positions. Reduced indinavir susceptibility was observed in 17 of 19 samples containing mutations at both positions 73 and 90 (89%) and in 16 of 18 samples with both 71 and 90 (89%) (See Table 10). The combination of mutations at position 90 with mutation at position 46 also 10 significantly increased the proportion of samples that had reduced indinavir susceptibility (Table 10).

15 (c) *Saquinavir susceptibility of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.*

Saquinavir resistance in viruses containing mutations at position 90 was evaluated with respect to the presence of other specific mutations. Decreased saquinavir susceptibility (fold-change in IC<sub>50</sub> greater than 2.5) in 20 viruses containing L90M but no other primary mutations was correlated with the presence of mutations at secondary positions. Reduced saquinavir susceptibility was observed in 15 of 19 samples containing mutations at both positions 73 and 90 (79%) and in 14 of 18 samples with both 71 and 25 90 (78%) (See Table 11). The combination of mutations at position 90 with mutations at other positions (e.g. 77 and 10) also significantly increased the proportion of samples that had reduced saquinavir susceptibility (Table 1).

30

35 (d) *Indinavir susceptibility of viruses containing combinations of mutations at amino acid 90 and many secondary mutations in HIV-1 Protease.*

Indinavir resistance in viruses containing mutations at

5 position 90 was evaluated with respect to the presence of  
a defined number of other mutations. Decreased indinavir  
susceptibility (fold-change in IC<sub>50</sub> greater than 2.5) in  
viruses containing L90M but no other primary mutations was  
correlated with the number of mutations at secondary  
10 positions. Reduced indinavir susceptibility was observed  
in 100% of samples with L90M and at least 5 other  
secondary mutations had (See Table 12). The proportion of  
samples that had reduced indinavir susceptibility  
increased significantly in samples with L90M combined with  
15 3 or 4 other secondary mutations (Table 12).

*(e) Saquinavir susceptibility of viruses containing  
combinations of mutations at amino acid 90 and many  
secondary mutations in HIV-1 Protease.*

20 Saquinavir resistance in viruses containing mutations at  
position 90 was evaluated with respect to the presence of  
a defined number of other mutations. Decreased saquinavir  
susceptibility (fold-change in IC<sub>50</sub> greater than 2.5) in  
viruses containing L90M but no other primary mutations was  
25 correlated with the number of mutations at secondary  
positions. Reduced saquinavir susceptibility was observed  
in 100% of samples with L90M and at least 5 other  
secondary mutations (See Table 12). The proportion of  
samples that had reduced saquinavir susceptibility  
30 increased significantly in samples with L90M combined with  
3 or 4 other secondary mutations (Table 12).

**EXAMPLE 9**

35 **Predicting Response to Protease Inhibitors by  
Characterization of Amino Acids 82 and 90 of HIV-1  
Protease.**

5

In one embodiment of this invention, changes in the amino acid at position 82 and 90 of the protease protein of HIV-1 are evaluated using the following method comprising: (i) collecting a biological sample from an HIV-1 infected 10 subject; (ii) evaluating whether the biological sample contains nucleic acid encoding HIV-1 protease having a valine to alanine (V82A), phenylalanine (V82F), serine (V82S), or threonine (V82T) substitution at codon 82 or a leucine to methionine at position 90 (L90M); and (iii) 15 determining susceptibility to protease inhibitors (PRI).

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such 20 as EDTA, acid citrate-dextrose, heparin), tissue biopsies, cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after 25 purification of virus particles from the biological sample. Evaluating whether the amino acid at position 82 of the HIV-1 protease is mutated to alanine, phenylalanine, serine, or threonine or at position 90 to methionine, can be performed using various methods, such 30 as direct characterization of the viral nucleic acid encoding protease or direct characterization of the protease protein itself. Defining the amino acid at positions 82 and 90 of protease can be performed by direct characterization of the protease protein by conventional 35 or novel amino acid sequencing methodologies, epitope recognition by antibodies or other specific binding

5 proteins or compounds. Alternatively, the amino acid at positions 82 and 90 of the HIV-1 protease protein can be defined by characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 nucleic acid can be performed using a variety  
10 of methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV protease at codons 82 and 90 can be determined by direct nucleic acid sequencing using various primer  
15 extension-chain termination (Sanger, ABI/PE and Visible Genetics) or chain cleavage (Maxam and Gilbert) methodologies or more recently developed sequencing methods such as matrix assisted laser desorption-ionization time of flight (MALDI-TOF) or mass spectrometry (Sequenom, Gene Trace Systems).  
20 Alternatively, the nucleic acid sequence encoding amino acid positions 82 and 90 can be evaluated using a variety of probe hybridization methodologies, such as genechip hybridization sequencing (Affymetrix), line probe assay  
25 (LiPA; Murex), and differential hybridization (Chiron).

In a preferred embodiment of this invention, evaluation of protease inhibitor susceptibility and of whether amino acid positions 82 and 90 of HIV-1 protease was wild type or alanine, phenylalanine, serine, or threonine in the case of position 82 and methionine at position 90, was carried out using a phenotypic susceptibility assay or genotypic assay, respectively, using resistance test vector DNA prepared from the biological sample. In one embodiment, plasma sample was collected, viral RNA was purified and an RT-PCR methodology was used to amplify a  
30  
35

5 patient derived segment encoding the HIV-1 protease and  
reverse transcriptase regions. The amplified patient  
derived segments were then incorporated, via DNA ligation  
and bacterial transformation, into an indicator gene viral  
vector thereby generating a resistance test vector.  
10 Resistance test vector DNA was isolated from the bacterial  
culture and the phenotypic susceptibility assay was  
carried out and analyzed as described in Example 1.

15 The nucleic acid (DNA) sequence of the patient derived  
HIV-1 protease and reverse transcriptase regions was  
determined using a fluorescence detection chain  
termination cycle sequencing methodology (ABI/PE). The  
method was used to determine a consensus nucleic acid  
sequence representing the combination of sequences of the  
20 mixture of HIV-1 variants existing in the subject sample  
(representing the quasispecies), and to determine the  
nucleic acid sequences of individual variants. Genotypes  
are analyzed as lists of amino acid differences between  
virus in the patient sample and a reference laboratory  
25 strain of HIV-1, NL4-3. Genotypes and corresponding  
phenotypes (fold-change in IC50 values) are entered in a  
relational database linking these two results with patient  
information. Large datasets can then be assembled from  
patient virus samples sharing particular characteristics,  
30 such as the presence of any given mutation or reduced  
susceptibility to any drug or combination of drugs.

**Protease inhibitor susceptibility of viruses containing  
mutations at amino acids 82 and 90 of HIV-1 Protease.**

35 Phenotypic susceptibility profiles of 33 patient virus  
samples which contained mutations at positions 82 (V82A,

5 F, S, or T) and 90 (L90M), but no other primary mutations, were analyzed. According to most published guidelines, such viruses are expected to be resistant to ritonavir, nelfinavir, indinavir, and saquinavir. However, 9% and 21% of these samples were phenotypically susceptible to 10 indinavir and saquinavir, respectively (see Table 6). Thus, particularly for saquinavir, there was poor correlation between the presence of mutations at positions 82 and 90 and drug susceptibility.

15

**EXAMPLE 10****Measuring Replication Fitness Using Resistance Test  
20 Vectors**

A means and method is provided for accurately measuring and reproducing the replication fitness of HIV-1. This method for measuring replication fitness is applicable to 25 other viruses, including, but not limited to hepadnaviruses (human hepatitis B virus), flaviviruses (human hepatitis C virus) and herpesviruses (human cytomegalovirus). This example further provides a means and method for measuring the replication fitness of HIV-1 that exhibits reduced drug susceptibility to reverse 30 transcriptase inhibitors and protease inhibitors. This method can be used for measuring replication fitness for other classes of inhibitors of HIV-1 replication, including, but not limited to integration, virus assembly, 35 and virus attachment and entry.

5      Replication fitness tests are carried out using the means and methods for phenotypic drug susceptibility and resistance tests described in US Patent Number 5,837,464 (International Publication Number WO 97/27319) which is hereby incorporated by reference.

10

In these experiments patient-derived segment(s) corresponding to the HIV protease and reverse transcriptase coding regions were either patient-derived segments amplified by the reverse transcription-polymerase 15 chain reaction method (RT-PCR) using viral RNA isolated from viral particles present in the serum of HIV-infected individuals or were mutants of wild type HIV-1 made by site directed mutagenesis of a parental clone of resistance test vector DNA. Resistance test vectors are 20 also referred to as "fitness test vectors" when used to evaluate replication fitness. Isolation of viral RNA was performed using standard procedures (e.g. RNAagents Total RNA Isolation System, Promega, Madison WI or RNAzol, Tel-Test, Friendswood, TX). The RT-PCR protocol was 25 divided into two steps. A retroviral reverse transcriptase [e.g. Moloney MuLV reverse transcriptase (Roche Molecular Systems, Inc., Branchburg, NJ), or avian myeloblastosis virus (AMV) reverse transcriptase, (Boehringer Mannheim, Indianapolis, IN)] was used to copy 30 viral RNA into cDNA. The cDNA was then amplified using a thermostable DNA polymerase [e.g. Taq (Roche Molecular Systems, Inc., Branchburg, NJ), Tth (Roche Molecular Systems, Inc., Branchburg, NJ), PrimeZyme (isolated from *Thermus brockianus*, Biometra, Gottingen, Germany)] or a 35 combination of thermostable polymerases as described for the performance of "long PCR" (Barnes, W.M., (1994) Proc.

5      Natl. Acad. Sci, USA 91, 2216-2220) [e.g. Expand High  
Fidelity PCR System (Taq + Pwo), (Boehringer Mannheim.  
Indianapolis, IN) OR GeneAmp XL PCR kit (Tth + Vent),  
(Roche Molecular Systems, Inc., Branchburg, NJ)].

10     PCR6 (Table 5, #1) is used for reverse transcription of  
viral RNA into cDNA. The primers, ApaI primer (PDSApa,  
Table 5, #2) and AgeI primer (PDSAge, Table 5, #3) used to  
amplify the "test" patient-derived segments contained  
sequences resulting in ApaI and AgeI recognition sites  
15     being introduced into both ends of the PCR product,  
respectively.

20     Fitness test vectors incorporating the "test"  
patient-derived segments were constructed as described in  
US Patent Number 5,837,464 (International Publication  
Number WO 97/27319) (see Fig. 1) using an amplified DNA  
product of 1.5 kB prepared by RT-PCR using viral RNA as a  
template and oligonucleotides PCR6 (#1), PDSApa (#2) and  
25     PDSAge (#3) as primers, followed by digestion with ApaI  
and AgeI or the isoschizomer PinAl. To ensure that the  
plasmid DNA corresponding to the resultant fitness test  
vector comprises a representative sample of the HIV viral  
quasi-species present in the serum of a given patient,  
30     many (>100) independent E. coli transformants obtained in  
the construction of a given fitness test vector were  
pooled and used for the preparation of plasmid DNA.

35     A packaging expression vector encoding an amphotrophic  
MuLV 4070A env gene product enables production in a  
fitness test vector host cell of fitness test vector viral

5 particles which can efficiently infect human target cells. Fitness test vectors encoding all HIV genes with the exception of env were used to transfect a packaging host cell (once transfected the host cell is referred to as a fitness test vector host cell). The packaging expression  
10 vector which encodes the amphotrophic MuLV 4070A env gene product is used with the resistance test vector to enable production in the fitness test vector host cell of infectious pseudotyped fitness test vector viral particles.

15 Fitness tests performed with fitness test vectors were carried out using packaging host and target host cells consisting of the human embryonic kidney cell line 293 (Cell Culture Facility, UC San Francisco, SF, CA)..

20 Fitness tests were carried out with fitness test vectors using two host cell types. Fitness test vector viral particles were produced by a first host cell (the fitness test vector host cell) that was prepared by transfecting a packaging host cell with the fitness test vector and the packaging expression vector. The fitness test vector viral particles were then used to infect a second host cell (the target host cell) in which the expression of the indicator gene is measured (see Fig. A).

30 The fitness test vectors containing a functional luciferase gene cassette were constructed and host cells were transfected with the fitness test vector DNA. The fitness test vectors contained patient-derived reverse  
35 transcriptase and protease DNA sequences that encode proteins which were either susceptible or resistant to the

5 antiretroviral agents, such as nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors and protease inhibitors.\_

10 The amount of luciferase activity detected in the infected cells is used as a direct measure of "infectivity", "replication capacity" or "fitness", i.e. the ability of the virus to complete a single round of replication. Relative fitness is assessed by comparing the amount of luciferase activity produced by patient derived viruses to 15 the amount of luciferase activity produced by a well-characterized reference virus (wildtype) derived from a molecular clone of HIV-1, for example NL4-3 or HXB2. Fitness measurements are expressed as a percent of the reference, for example 25%, 50%, 75%, 100% or 125% of 20 reference (Figure B, C).

Host cells were seeded in 10-cm-diameter dishes and were transfected one day after plating with fitness test vector plasmid DNA and the envelope expression vector. 25 Transfections were performed using a calcium-phosphate co-precipitation procedure. The cell culture media containing the DNA precipitate was replaced with fresh medium, from one to 24 hours, after transfection. Cell culture media containing fitness test vector viral 30 particles was harvested one to four days after transfection and was passed through a 0.45-mm filter before being stored at -80°C. HIV capsid protein (p24) levels in the harvested cell culture media were determined by an EIA method as described by the manufacturer (SIAC; 35 Frederick, MD). Before infection, target cells (293 and 293/T) were plated in cell culture media. Control

5 infections were performed using cell culture media from  
mock transfections (no DNA) or transfections containing  
the fitness test vector plasmid DNA without the envelope  
expression plasmid. One to three or more days after  
infection the media was removed and cell lysis buffer  
10 (Promega) was added to each well. Cell lysates were  
assayed for luciferase activity. Alternatively, cells  
were lysed and luciferase was measured by adding Steady-  
Glo (Promega) reagent directly to each well without  
aspirating the culture media from the well.

15

**Example 11****Measuring Replication Fitness of Viruses with  
Deficiencies in Reverse Transcriptase Activity**

20 A means and method is provided for identifying mutations  
in reverse transcriptase that alter replication fitness.  
A means and method is provided for identifying mutations  
that alter replication fitness and can be used to identify  
mutations associated with other aspects of HIV-1  
25 replication, including, but not limited to integration,  
virus assembly, and virus attachment and entry. This  
example also provides a means and method for quantifying  
the affect that specific mutations reverse transcriptase  
have on replication fitness. A means and method for  
30 quantifying the affect that specific protease and reverse  
transcriptase mutations have on replication fitness to  
mutations in other viral genes involved in HIV-1  
replication, including, but not limited to the gag, pol,  
and envelope genes is also provided.

35

Fitness test vectors were constructed as described in

5 example 10. Fitness test vectors derived from patient samples or clones derived from the fitness test vector pools, or fitness test vectors were engineered by site directed mutagenesis to contain specific mutations, and were tested in a fitness assay to determine accurately and  
10 quantitatively the relative fitness compared to a well-characterized reference standard. A patient sample was examined for increased or decreased reverse transcriptase activity and correlated with the relative fitness observed (Figure C).

15 **Reverse transcriptase activity of patient HIV samples**

Reverse transcriptase activity can be measured by any number of widely used assay procedures, including but not limited to homopolymeric extension using (e.g. oligo dT:poly rC) or real time PCR based on molecular beacons (reference Kramer) or 5' exonuclease activity (Lie and Petropoulos, 1996). In one embodiment, virion associated reverse transcriptase activity was measured using a quantitative PCR assay that detects the 5' exonuclease activity associated with thermo-stable DNA polymerases (Figure C). In one embodiment of the invention, the fitness of the patient virus was compared to a reference virus to determine the relative fitness compared to "wildtype" viruses that have not been exposed to reverse transcriptase inhibitor drugs. In another embodiment, the fitness of the patient virus was compared to viruses collected from the same patient at different timepoints, for example prior to initiating therapy, before or after changes in drug treatment, or before or after changes in virologic (RNA copy number), immunologic (CD4 T-cells), or 30 clinical (opportunistic infection) markers of disease progression.

5

**Genotypic analysis of patient HIV samples**

Fitness test vector DNAs, either pools or clones, are analyzed by any of the genotyping methods described in Example 1. In one embodiment of the invention, patient 10 HIV sample sequences were determined using viral RNA purification, RT/PCR and ABI chain terminator automated sequencing. The sequence was determined and compared to reference sequences present in the database or compared to a sample from the patient prior to initiation of therapy. 15 The genotype was examined for sequences that are different from the reference or pre-treatment sequence and correlated to the observed fitness.

**Fitness analysis of site directed mutants**

20

Genotypic changes that are observed to correlate with changes in fitness were evaluated by construction of fitness vectors containing the specific mutation on a defined, wild-type (drug susceptible) genetic background. 25 Mutations may be incorporated alone and/or in combination with other mutations that are thought to modulate the fitness of a virus. Mutations were introduced into the fitness test vector through any of the widely known methods for site-directed mutagenesis. In one embodiment 30 of this invention the mega-primer PCR method for site-directed mutagenesis is used. A fitness test vector containing the specific mutation or group of mutations were then tested using the fitness assay described in Example 10 and the fitness was compared to that of a 35 genetically defined wild-type (drug susceptible) fitness test vector which lacks the specific mutations. Observed

5 changes in fitness are attributed to the specific mutations introduced into the resistance test vector. In several related embodiments of the invention, fitness test vectors containing site directed mutations in reverse transcriptase that result in amino acid substitutions at 10 position 190 (G190A, G190S, G190C, G190E, G190V, G190T) and that display different amounts of reverse transcriptase activity were constructed and tested for fitness (Figure D). The fitness results were correlated with specific reverse transcriptase amino acid 15 substitutions and fitness.

**Example 12**

**Measuring Replication Fitness of Viruses with Deficiencies in Protease Activity**

20 A means and method for identifying mutations in protease that alter replication fitness is provided.

25 This example provides the means and methods for identifying mutations that alter replication fitness for various components of HIV-1 replication, including, but not limited to integration, virus assembly, and virus attachment and entry. This example also provides a means and method for quantifying the affect that specific 30 mutations in protease or reverse transcriptase have on replication fitness. This method can be used for quantifying the effect that specific protease mutations have on replication fitness and can be used to quantify the effect of other mutations in other viral genes 35 involved in HIV-1 replication, including, but not limited to the gag, pol, and envelope genes.

5

Fitness test vectors were constructed as described in example 10. Fitness test vectors derived from patient samples or clones derived from the fitness test vector pools, or fitness test vectors engineered by site directed 10 mutagenesis to contain specific mutations, were tested in a fitness assay to determine accurately and quantitatively the relative fitness compared to a well-characterized reference standard. A patient sample was examined further for increased or decreased protease activity correlated 15 with the relative fitness observed (Figure C).

**Protease activity of patient HIV samples**

Protease activity can be measured by any number of widely used assay procedures, including but not limited to in 20 vitro reactions that measure protease cleavage activity (reference Erickson ). In one embodiment, protease cleavage of the gag polyprotein (p55) was measured by Western blot analysis using an anti-capsid (p24) antibody 25 (Figure C). In one embodiment of the invention, the fitness of the patient virus was compared to a reference virus to determine the relative fitness compared to "wildtype" viruses that have not been exposed to protease inhibitor drugs. In another embodiment, the fitness of the patient virus was compared to viruses collected from 30 the same patient at different timepoints, for example prior to initiating therapy, before or after changes in drug treatment, or before or after changes in virologic (RNA copy number), immunologic (CD4 T-cells), or clinical (opportunistic infection) markers of disease progression.

35

**Genotypic analysis of patient HIV samples**

5      Fitness test vector DNAs, either pools or clones, are  
analyzed by any of the genotyping methods described in  
Example 1. In one embodiment of the invention, patient  
HIV sample sequences were determined using viral RNA  
purification, RT/PCR and ABI chain terminator automated  
10     sequencing. The sequence was determined and compared to  
reference sequences present in the database or compared to  
a sample from the patient prior to initiation of therapy,  
if available. The genotype was examined for sequences  
that are different from the reference or pre-treatment  
15     sequence and correlated to the observed fitness.

**Fitness analysis of site directed mutants**

20     Genotypic changes that are observed to correlate with  
changes in fitness are evaluated by construction of  
fitness vectors containing the specific mutation on a  
defined, wild-type (drug susceptible) genetic background.  
Mutations may be incorporated alone and/or in combination  
25     with other mutations that are thought to modulate the  
fitness of a virus. Mutations are introduced into the  
fitness test vector through any of the widely known  
methods for site-directed mutagenesis. In one embodiment  
of this invention the mega-primer PCR method for  
site-directed mutagenesis is used. A fitness test vector  
30     containing the specific mutation or group of mutations are  
then tested using the fitness assay described in Example  
10 and the fitness is compared to that of a genetically  
defined wild-type (drug susceptible) fitness test vector  
which lacks the specific mutations. Observed changes in  
35     fitness are attributed to the specific mutations  
introduced into the fitness test vector. In several

5 related embodiments of the invention, fitness test vectors containing site directed mutations in reverse protease that result in amino acid substitutions at positions 30, 10 63, 77, 90 (list from Figure E) and that display different amounts of protease activity are constructed and tested for fitness (Figure E). The fitness results enable the correlation between specific protease amino acid substitutions and changes in viral fitness.

#### Example 13

15 **Measuring Replication Fitness and Drug Susceptibility in a Large Patient Population**

This example describes the high incidence of patient samples with reduced replication fitness. This example 20 also describes the general correlation between reduced drug susceptibility and reduced replication fitness. This example further describes the occurrence of viruses with reduced fitness in patients receiving protease inhibitor and/or reverse transcriptase inhibitor treatment. This 25 example further describes the incidence of patient samples with reduced replication fitness in which the reduction in fitness is due to altered protease processing of the gag polyprotein (p55). This example further describes the incidence of protease mutations in patient samples that 30 exhibit low, moderate or normal (wildtype) replication fitness. This example further describes protease mutations that are frequently observed, either alone or in combination, in viruses that exhibit reduced replication capacity. This example also describes the incidence of 35 patient samples with reduced replication fitness in which the reduction in fitness is due to altered reverse

5 transcriptase activity. This example describes the occurrence of viruses with reduced replication fitness in patients failing antiretroviral drug treatment.

10 Fitness/resistance test vectors were constructed as described in example 10. Fitness and drug susceptibility was measured in 134 random patient samples that were received for routing phenotypic testing by the ViroLogic Clinical Reference Laboratory. Fitness assays were performed as described in Example 10. Drug susceptibility 15 testing and genotyping of the protease region was performed as described in Example 1. Reverse transcriptase activity was measured as described in Example 11. Protease processing was measured as described in Example 12.

20

**Drug susceptibility of patient viruses**

Reduced drug susceptibility was observed for a majority of the patient virus samples (Table A). 66 percent of the viruses exhibited large (define as >10X of the reference) 25 reductions in susceptibility to one or more NRTI drugs. 52 percent of the viruses exhibited large reductions in susceptibility to one or more NNRTI drugs. 45 percent of the viruses exhibited large reductions in susceptibility to one or more PRI drugs.

30

**Fitness of patient viruses**

Reduced replication fitness was observed for a majority of the patient virus samples (Table A). Forty one percent of the viruses exhibited large reductions in replication 35 fitness (<25% of the reference). Another 45% had moderate reductions (between 25-75% of the reference) in

5 replication fitness. A minority of the patient samples (14%) displayed replication fitness that approached or exceeded "wildtype" levels (>75% of the reference). Viruses with reduced drug susceptibility, were much more likely to display reduced replication fitness (Figures F,  
10 G, H, and I).

**Protease Mutations in patient viruses**

Greater than 10 mutations in protease were observed in a majority of the patient virus samples (Table A). Viruses  
15 with reduced fitness were much more likely to contain 10 or more protease mutations (Figure I). Sixty two percent of the viruses that exhibited large reductions in replication fitness (<25% of the reference) contained 10 or more protease mutations. Twenty two percent of the viruses with moderate reductions (between 25-75% of the reference) in fitness contained 10 or more protease mutations. Only 5% of the viruses that displayed replication fitness that approached or exceeded "wildtype" levels (>75% of the reference) contained 10 or more  
20 protease mutations (Table A). Certain protease mutations either alone (D30N) or in combination (L90M plus K20T, or M46I, or T3, or N88D) were observed at high incidences in viruses with reduced fitness (Figures I and J).

30 **Protease processing of patient viruses**

Reduced protease processing of the p55 gag polyprotein was observed in a majority of the patient virus samples (Table A). Viruses with reduced fitness were much more likely to display reduced protease processing; defined as having

5 detectable amounts of the p41 intermediate cleavage product (Figures F, I and K). Seventy one percent of the viruses that exhibited large reductions in replication fitness (<25% of the reference) displayed reduced protease processing. Eighteen percent of the viruses with moderate 10 fitness reductions (between 25-75% of the reference) displayed reduced protease processing. Only 10% of the viruses that displayed replication fitness that approached or exceeded "wildtype" levels (>75% of the reference) exhibited reduced protease processing (Table A). Certain 15 protease mutations (D30N, M46I/L, G48V, I54L/A/S/T/V, and I84V) were observed at high incidences in viruses with reduced protease processing of the p55 gag polyprotein (Figure L).

20 **Reverse transcriptase of patient viruses**

Reduced reverse transcriptase activity processing was observed in a minority of the patient virus samples (Table A). Viruses with reduced fitness were much more likely to display reduced reverse transcriptase activity. Fourteen 25 percent of the viruses that exhibited large reductions in replication fitness (<25% of the reference) displayed reduced reverse transcriptase activity. Only 2% of the viruses with moderate fitness reductions (between 25-75% of the reference) displayed reduced reverse transcriptase activity. 30 None of the viruses that displayed replication fitness that approached or exceeded "wildtype" levels (>75% of the reference) exhibited reduced reverse transcriptase activity.

5

**Example 14****Measuring Replication Fitness to Guide Treatment Decisions**

A means and method for using replication fitness measurements to guide the treatment of HIV-1 is provided. 10 This example further provides a means and method for using replication fitness measurements to guide the treatment of patients failing antiretroviral drug treatment. This example further provides the means and methods for using replication fitness measurements to guide the treatment of 15 patients newly infected with HIV-1.

**Guiding treatment of patients with multi-drug resistant virus:** Fitness/resistance test vectors were constructed as described in example 10. Fitness and drug susceptibility 20 were measured on serial longitudinal samples collected weekly for 12 weeks from 18 patients. These patients were considered failing a protease inhibitor (typically indinavir) containing regimen and had incomplete suppression of virus replication based on routine viral 25 load testing (>2,500 copies/mL). Phenotypic drug susceptibility testing indicated that these patient viruses were multi-drug resistant. Each patient agreed to interrupt therapy for a period of at least 12 weeks. Phenotypic drug susceptibility assays were performed as 30 described in Example 1 on serial samples collected just prior to interrupting therapy and weekly during the period of interruption. Fitness assays were performed as described in Example 10 on serial samples collected just prior to interrupting therapy and weekly during the period

5 of interruption. Protease processing was measured as described in Example 12.

10 Of the 18 patients that interrupted therapy, 16 patients had resistant viruses that regained susceptibility to antiretroviral drugs during the period of treatment interruption. The phenotypic test results of a representative patient are shown in Figure M. Typically, 15 susceptibility returned to all drug classes simultaneously, consistent with the re-emergence of a minor population of drug sensitive virus. In the representative example shown in Figure M, drug sensitivity was abruptly restored between weeks 9 and 10. Genotypic analysis (DNA sequence of protease and reverse transcriptase) are also consistent with the re-emergence 20 of a drug sensitive virus. These data show the loss of most or all drug resistance mutation simultaneously (data not shown). The data are not consistent with random back mutations. Back mutations would predict that restored susceptibility to drugs would occur unevenly for different 25 drug classes and/or within a drugs within the same class.

30 Generally, the re-emergence of the drug susceptible virus was also accompanied by a simultaneous increase in replication fitness. This relationship is clearly evident for the representative virus (Figure N). Several other examples with less frequent timepoints are shown in Figure O. Virus from patients that did not revert to drug susceptibility after interruption generally did not exhibit an increase in replication fitness, nor did

5      viruses from patients that did not interrupt treatment (Figures 0). The data indicate that the drug sensitive virus that re-emerged after treatment interruption is able to replicate better than the drug resistant virus that was present before treatment was interrupted. The re-  
10     emergence of drug susceptible virus in this group of patients was also accompanied by an increase in viral load and a decrease in DC4 T-cells, indicators of disease progression. Thus, fitness information can be used to guide treatment of patients that harbor multi-drug  
15     resistant virus and are considering treatment interruption. If the patient virus is drug resistant but has low replication capacity, the patient and the physician should consider continuing drug treatment to prevent the re-emergence of a drug sensitive virus with  
20     higher replication capacity and greater pathogenicity. Alternatively, if the patient virus is drug resistant and has high replication capacity, the patient and the physician may consider interrupting treatment to spare the patient from the harmful and unpleasant side effects of  
25     antiretroviral drugs that are not providing clinical benefit.

Furthermore, physicians may choose to perform routine replication fitness assays for patients that have multi-  
30     drug resistant virus. This assay could be used to monitor the replication fitness of patient viruses when complete suppression of virus replication is not possible due to multi-drug resistance. The assay would be used to guide treatment decisions that prevent the drug resistant virus

5 with low replication fitness from increasing its replication fitness. In this way, physicians may prolong the usefulness of antiretroviral drugs despite the presence of drug resistant virus in the patient.

10 **Guiding treatment of newly infected patients:**

Patients that maintain high virus loads (setpoint) after acute infection are more likely to exhibit accelerated disease progression. Therefore, it is advantageous for 15 this class of patient to initiate antiretroviral drug treatment as soon as possible after diagnosis with HIV-1 infection. In conjunction with viral load, fitness measurements of viruses in newly infected patients may provide a useful measurement to identify those individuals 20 that will develop elevated setpoints after primary infection and consequently are likely to exhibit accelerated disease progression. Fitness measurements may guide the decision to treat immediately after diagnosis or a some later time point.

25

**Example 15**

**Measuring Saquinavir Susceptibility of Viruses Containing Various Amino Acid Substitutions in Protease at Position 82**

30

This example provides a means and method for identifying mutations in protease that affect susceptibility (increased or decreased) to saquinavir.

5 In one embodiment of this invention, the effects of combination of mutations at position 82 (for example, V82A, V82F, V82S, or V82T) are evaluated using the following method comprising: (i) collecting a biological sample from an HIV-1 infected subject; (ii) evaluating  
10 whether the HIV-1 in the sample contains nucleic acid encoding protease having a valine to alanine (V82A), phenylalanine (V82F), serine (V82S), or threonine (V82T) substitution at position 82 or a leucine to methionine substitution at position 90 (L90M); and (iii) determining  
15 susceptibility to protease inhibitors (PRIs).

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after  
20 purification of virus particles from the biological sample. Evaluating whether the amino acid at position 82 of the HIV-1 protease is mutated to alanine, phenylalanine, or threonine, can be performed using various methods, such as direct characterization of the  
25 viral nucleic acid encoding protease or direct characterization of the protease protein itself. Defining the amino acid at position 82 of protease can be performed by direct characterization of the protease protein by conventional or novel amino acid sequencing methodologies,

5 epitope recognition by antibodies or other specific binding proteins or compounds. Alternatively, the amino acid at position 82 of the HIV-1 protease protein can be defined by characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification  
10 of the HIV-1 nucleic acid can be performed using a variety of methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV protease at codon 82 can be determined by direct nucleic acid sequencing using various primer extension-chain  
15 termination (Sanger, ABI/PE and Visible Genetics) or chain cleavage (Maxam and Gilbert) methodologies or more recently developed sequencing methods such as matrix assisted laser desorption-ionization time of flight (MALDI-TOF) or mass spectrometry (Sequenom, Gene Trace Systems). Alternatively, the nucleic acid sequence encoding amino acid position 82 can be evaluated using a variety of probe hybridization methodologies, such as genechip hybridization sequencing (Affymetrix), line probe  
20 assay (LiPA; Murex), and differential hybridization  
25 (Chiron).

In a preferred embodiment of this invention, evaluation of  
30 the effects of mutations at amino acid position 82 of HIV-1 protease on protease inhibitor susceptibility, was carried out using a phenotypic susceptibility assay using resistance test vector DNA prepared from the biological sample. In one embodiment, plasma samples were collected,

5     viral RNA was purified and an RT-PCR methodology was used  
to amplify a patient derived segment encoding the HIV-1  
protease and reverse transcriptase regions. The amplified  
patient derived segments were then incorporated, via DNA  
ligation and bacterial transformation, into an indicator  
10    gene viral vector thereby generating a resistance test  
vector. Resistance test vector DNA was isolated from the  
bacterial culture and the phenotypic susceptibility assay  
was carried out as described in Example 1. The genotype of  
the protease region was determined by dideoxy chain-  
15    termination sequencing of the resistance test vector DNA.  
The results are summarized for saquinavir (SQV) in Figure  
6. Samples were categorized as having mutations in  
protease encoding alanine (A), phenylalanine (F), or  
threonine (T) at position 82, instead of the wild-type  
20    valine (V), and the percentage of samples in each category  
displaying hyper-sensitivity to saquinavir (i.e., fold-  
change vs. reference of 0.4 or less) was determined.  
Surprisingly, the percentage of saquinavir hyper-  
susceptible viruses was much higher amongst viruses  
25    containing V82F than those containing V82A or V82T. This  
observation implies that the detection of V82F in protease  
predicts a positive virological response to saquinavir  
treatment.

**Example 16****Measuring Replication Fitness of Viruses with  
Mutations in Integrase**

10 This example provides a means and method for identifying mutations in integrase that alter replication fitness.

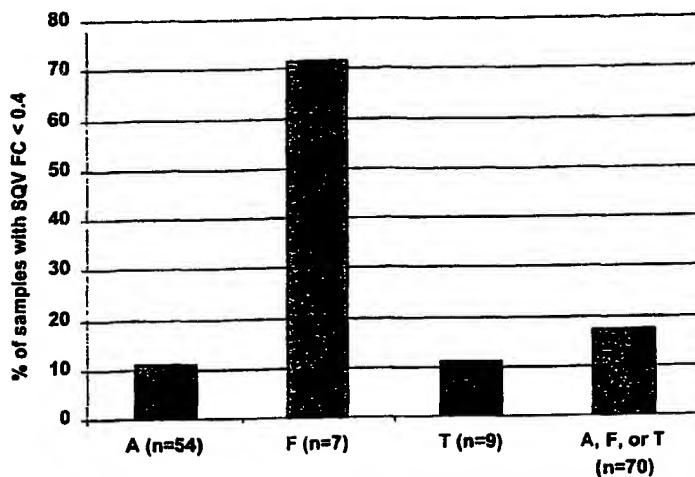
This example provides the means and methods for identifying mutations that alter replication fitness for various components of HIV-1 replication, including, but not limited to integration, virus assembly, and virus attachment and entry. This example also provides a means and method for quantifying the affect that specific mutations in protease, reverse transcriptase, or integrase have on replication fitness. This method can be used for quantifying the effect that specific integrase mutations have on replication fitness and can be used to quantify the effect of other mutations in other viral genes involved in HIV-1 replication, including, but not limited 25 to the gag, pol, and envelope genes.

Fitness test vectors engineered by site directed mutagenesis to contain specific mutations in integrase were tested in a fitness assay to determine accurately and 30 quantitatively the relative fitness compared to a well-characterized reference standard.

Genotypic changes that are observed to correlate with resistance to integrase inhibitors are evaluated by

5 construction of fitness vectors containing the specific mutation on a defined, wild-type (drug susceptible) genetic background. Mutations may be incorporated alone and/or in combination with other mutations that are thought to modulate the fitness of a virus. Mutations  
10 are introduced into the fitness test vector through any of the widely known methods for site-directed mutagenesis. In one embodiment of this invention the mega-primer PCR method for site-directed mutagenesis is used (Sarkar, G. and Sommar, S.S., 1994, *Biotechniques* 8, 404-407). A  
15 fitness test vector containing the specific mutation or group of mutations are then tested using the fitness assay described in Example 10 and the fitness is compared to that of a genetically defined wild-type (drug susceptible) fitness test vector which lacks the specific mutations.  
20 Observed changes in fitness are attributed to the specific mutations introduced into the fitness test vector. In several related embodiments of the invention, fitness test vectors containing site directed mutations in integrase that result in amino acid substitutions at positions 66,  
25 154, 66 and 153, and 66 and 154 are constructed and tested for fitness (Figure 7). As controls, mutants with multiple changes conferring resistance to reverse transcriptase and protease inhibitors (MDRC4) and with a mutation in the integrase active site (D64V) were also  
30 tested. The fitness results enable the correlation between specific integrase amino acid substitutions and changes in viral fitness.

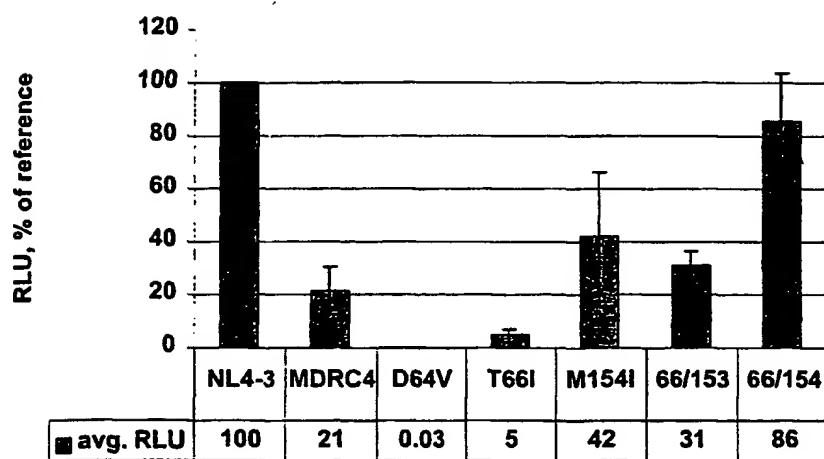
5      Figure 6. Distribution of saquinavir hyper-susceptibility by amino acid change at position 82.



10

5

Figure 7. Relative luciferase activity of integrase inhibitor-resistant site-directed mutants.



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25 Table 1: PRI susceptibility of selected patient samples. Viruses displaying increased susceptibility to amprenavir (5-fold or greater) were genotyped and found to contain the N88S mutation in PR. Samples were listed in order of decreasing amprenavir susceptibility.

Table 1

Sample ID	Prior PRI Experience	Fold Change vs. Reference					PR Mutations
		SQV	IDV	RTV	NFV	AMP	
0732	NFV	0.73	2.11	1.72	0.91	0.08	K14R, I15V, K20T, E35D, M36I, R41K, I62V, L63Q, N88S
627	IDV	0.26	0.16	1.50	21.00	0.09	I131V, E35D, M46L, L63P, I64V, I73V, N88S
1208	NFV	1.55	3.15	1.22	0.96	0.10	I62V, L63P, V77I, N88S
360	IDV	1.88	0.31	1.49	29.95	0.15	I13V, K20M, M36V, N37A, M46I, I62V, L63P, N88S, I93L
0910	NFV	1.41	5.47	1.85	14.70	0.16	M46I, L63P, V77I, N88S, I93L
3542	IDV	1.28	7.61	3.16	24.67	0.16	I13V, K14R, N37D, M46I, L63P, N88S, I93L
3654		1.80	7.56	1.95	18.61	0.20	I13V, R41K, M46I, L63P, V77I, N88S, I93L

Fold Change Limit: **2.5** **20.4**

5 Table 2: PRI susceptibility of site-directed mutants in PR. Mutations were introduced into the drug sensitive reference resistance test vector and the susceptibility to PRIs was determined.

Table 2

Site-Directed Mutations	Fold Change vs. reference				
	SQV	IDV	RTV	NFV	AMP
L63P	1.04	1.12	1.27	1.43	1.06
L63P, V77I	1.24	1.72	1.73	2.49	0.91
N88S	0.47	1.56	0.36	2.39	0.04
L63P, N88S	1.44	2.56	0.77	5.10	0.11
L63P, V77I, N88S	1.24	3.09	1.39	1.239	0.08
M46L, L63P, N88S	1.15	2.30	0.85	6.18	0.12
M46L, L63P, V77I, N88S	1.45	2.97	1.33	12.24	0.14

FOLD CHANGE LIMITS: &lt;0.4 &gt;2.5

5

Table 3: Relative luciferase activity levels for patient sample virus-derived resistance test vector pools. The luciferase activity (relative light units, RLU) measured in the absence of drug for the patient sample was compared to that of the drug sensitive reference control from the same assay run, and expressed as a percentage of control. These values are from one assay each. All the samples that contain the N88S mutations in PR were found to have reduced luciferase activity compared to control.

10  
15

Table 3

Sample ID	PR Mutations	Relative Luciferase Activity (% of control)
0732	K14R, I15V, K20T, E35D, M36I, R41K, I62V, L63Q, N88S	8.5
627	I13I/V, E35D, M46L, L63P, I64V, I73V, N88S	0.7
1208	I62V, L63P, V77I, N88S	14.2
360	I13V, K20M, M36V, N37A, M46I, I62V, L63P, N88S, I93L	2.2
0910	M46I, L63P, V77I, N88S, I93L	16.0
3542	I13V, K14R, N37D, M46I, L63P, N88S, I93L	4.6
3654	I13V, R41K, M46I, L63P, V77I, N88S, I93L	12.8

5

Table 4: Relative luciferase activity levels for resistance test vectors containing site-directed mutations. The luciferase activity (relative light units, RLU) measured in the absence of drug for the mutant was compared to that of the drug sensitive reference control from the same assay run, and expressed as a percentage of control. These values are from one to five assays each, and each value was obtained using an independent clone for mutants which were tested multiple times. All the constructs that contain the N88S mutations in PR were found to have reduced luciferase activity compared to control. All the constructs with the K20T mutation were essentially inactive in the assay.

Table 4

Site-Directed Mutations	Average Luciferase Activity (% of control)	number of clones tested
L63P	163.9	1
L63P, V77I	75.6	1
N88S	1.0	3
L63P, N88S	20.7	2
L63P, V77I, N88S	29.3	2
M46L, L63P, N88S	28.0	2
M46L, L63P, V77I, N88S	53.2	5
K20T, N88S	<0.01	5
K20T, L63P, N88S	<0.01	1

5      Table 5: Oligonucleotide primers used for PCR  
amplification and for generating site-directed mutants.

10

Table 5.

Primer name:			
#1: PCR6	5'	CCAAATTTRYTGATATTTCTCATGNCTCTGGG	3' (35-mer)
#2: PDS/Aps	5'	CATGGTGAGGGCCCTAGGAAAAGGGCTGGAAATGTG	3' (42-mer)
#3: PDS/Age	5'	CACTCCATGTACCGGTTCTTAAAGAATYTCYCTG	3' (34-mer)
#4: RzII	5'	ACTTTGGACCGTCCATTCTGGCTTAATTAACTGGTACAG	3' (43-mer)
#5: K20T	5'	GGGGGGCAATTAAACGGAAGCTCTATTAG	3' (28-mer)
#6: M46L	5'	GATGGAAACCAAATTGATAGGGGAATTG	3' (30-mer)
#7: L63P	5'	GTATGATCAGATAACCATAGAAATCTGC	3' (28-mer)
#8: N88S	5'	CTGAGTCAACAGACTCTTCCAATTATG	3' (28-mer)

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R = A or G  
Y = C or T  
N = A, C, G, or T  
H = A, C, or T

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30

35      Table 6. PRI Susceptibility (Fold Change <2.5) of Viruses  
with Mutations at 82 and/or 90

Percent of viruses with indicated primary  
mutation(s) which are drug sensitive (fold  
change in IC50 < 2.5)

drug	V82A/F/S/T	L90M	V82A/F/S/T and L90M
RTV	8.0	27.6	3.0
NFV	20.0	8.6	3.0
40      IDV	22.7	31.0	9.1
AMP	53.3	65.5	33.3
SQV	73.3	46.6	21.2

**Table 7. Correlation Between 82A/F/S/T, Secondary Mutations, and IDV Susceptibility.**

	position	n	% FC > 2.5	chi square p
10	24	20	100%	<0.005
	71	27	100%	<0.0001
	54	38	95%	<0.0001
	46	35	89%	<0.01
15	10	47	83%	<0.05
	63	72	79%	<0.05
	82	75	77%	

20 all virus with V82A/F/S/T and no other primary mutations.

5      **Table 8. Correlation Between 82A/F/S/T, Secondary  
Mutations, and SQV Susceptibility.**

	position	n	% FC > 2.5	chi square p
10	20	5	80%	<0.001
	36	11	73%	<0.001
	24	20	65%	<0.0001
	71	27	52%	<0.0001
	54	38	47%	<0.0001
	10	47	40%	<0.001
15	82	75	27%	

all virus

20      **Table 9. Association Between SQV and IDV Susceptibility,  
V82A/F/S/T, and Number of Resistance Associated Mutations**

	Number of secondary mutations	Number of samples	% with IDV FC > 2.5	% with SQV FC > 2.5
25	1	75	77	27
	2	67	82	30
	3	51	88	39
	4	38	95	50
	5	25	96	60
	6	17	100	76
	7	5	100	60

5

**Table 10. Correlation Between L90M, Secondary Mutations, and IDV Susceptibility.**

10	<u>position</u>	<u>n</u>	<u>% FC &gt; 2.5</u>	<u>chi square p</u>
	73	19	89%	<0.01
	71	18	89%	<0.001
	46	25	88%	<0.05
	90	58	69%	

15

all viruses with L90M and

**Table 11. Correlation Between L90M, Secondary Mutations, and SQV Susceptibility.**

20	<u>position</u>	<u>n</u>	<u>% FC &gt; 2.5</u>	<u>chi square p</u>
	73	19	79%	<0.01
	71	18	78%	<0.001
	77	25	76%	<0.05
	10	34	65%	<0.05
25	90	58	55%	

all viruses

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5           Table 12. Association Between SQV and IDV  
Susceptibility, L90M, and Number of Resistance Associated  
Mutations.

	Number of secondary mutations	Number of samples	% w with IDV FC > 2.5	% w FC > 2.5	with SQV
10	0	58	69	53	
	1	57	70	47	
	2	56	70	48	
	3	41	80	68	
	4	31	87	77	
	5	14	100	100	
	6	6	100	100	

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Summary of the Invention

- In another embodiment of this invention, a method is provided of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
  - 5 (a) collecting a biological sample from the HIV-infected patient;
  - (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 84, 48, 23, 73, 53, 33, 74, 20, 90, 32 and 39 or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 66, 84, 54, 48, 33, 73, 15 20, 71, 64 and 93, and
  - (c) determining a change in susceptibility to a protease inhibitor, wherein the protease inhibitor is saquinavir.

20 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 84, 48, 23, 73, 53, 33, 74, 20, and 90, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 66, 84, 54, 48, 33, 73, 25 20, and 71, wherein the change in susceptibility in step (c) is a decrease in susceptibility to saquinavir.

30 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and

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a secondary mutation at codons 32 or 39, or a mutation at codon 90 and a secondary mutation at codons 64 or 93, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

5

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 90 and a secondary mutation at codons selected from the group 10 consisting of 53, 95, 54, 84, 82, 46, 13, and 74, wherein the protease inhibitor is indinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease 15 antiretroviral therapy, having a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, and 46, wherein the change in susceptibility in step (c) is a decrease in susceptibility to indinavir.

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In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 90 and a secondary mutation at codons 13 or 74, wherein the 25 change in susceptibility in step (c) is an increase in susceptibility to indinavir.

30

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 48, 23, 84, 53, 74, 60, 33, 36, 35, 32, and 46 or a mutation at codon

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90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, 62, 74, 53, 48, 23, 58, 36, 64, 77, and 93.

5 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

10 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein step (c) is determining a change in susceptibility to the protease inhibitor greater than 10 fold.

15 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 48, 23, 84, 53, 74, 20, 60, 33, 36, 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 84, 53, 48, 23, 58, 20, 36, and 54, wherein the change in susceptibility in step (c) is a decrease in susceptibility to saquinavir.

20 In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codons 32 or 46, or a mutation at codon 90 and a secondary mutation at codons 64, 77, or 93, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and 5 a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, and 90, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, and 62, wherein the change in susceptibility 10 in step (c) is a decrease in susceptibility to indinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codon 13, or a mutation at codon 15 90 and a secondary mutation at codon 74, wherein the change in susceptibility in step (c) is an increase in susceptibility to indinavir.

In another embodiment of this invention, a method is 20 provided of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

- (a) collecting a biological sample from the HIV-infected patient;
- 25 (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and secondary mutations of at least three codons; and
- (c) determining a decrease in susceptibility to 30 saquinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease

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antiretroviral therapy, wherein in the evaluating step (b), the nucleic acid encoding HIV protease has secondary mutations of at least five codons.

5       In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the secondary mutation are selected from the group consisting of codons 10, 20, 52, 53, 54, 66, 71, 73 and 84.

10      In another embodiment of this invention, a method is provided of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

15      (a) collecting a biological sample from the HIV-infected patient;

16      (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 33, 23, 84, 32, 53, 90, 37, 71, 46, 10, 54, 61, 11, and 46, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 74, 25 15, 47, 66, 32, 55, 53, 13, and 69; and

26      (c) determining a change in susceptibility to amprenavir.

30      In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F),

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serine (S), or threonine (T) for valine(V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

5       In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 33, 23, 84, 32, 53, 90, 37, 71, 46, 10, 54, 10      11, and 46, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 47, 66, 32, 55, 53, and 13; wherein the change in susceptibility in step (c) is a decrease in susceptibility 15      to saquinavir.

In another embodiment of this invention, the above method is provided of assessing the effectiveness of protease antiretroviral therapy, having a mutation at codon 82 and a secondary mutation at codon 61, or a mutation at codon 20      90 and secondary mutations at codons 74, 15, or 69, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

25      In another embodiment of this invention, a resistance test vector is provided comprising an HIV patient-derived segment comprising nucleic acid encoding protease having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 73, 55, 48, 20, 43, 30      53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and secondary mutations at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71,

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64, 93, 23, 58, and 36 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient-derived segment.

5 In another embodiment of this invention, the above resistance test vector is provided, wherein the mutation of the patient derived segment at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V) and the mutation at 10 codon 90 is a substitution of methionine (M) for leucine (L).

**Phenotypic Susceptibility:**

15 Phenotypic assays provide information relating to drug resistance in the form of a fold-change in IC50 value, i.e. the ratio of the IC50 for the patient virus to that of a drug sensitive reference control. The significance of the fold change value with respect to treatment choices is limited by at least two factors: the reproducibility of 20 the assay, and the achievable drug concentration at the site of action in the patient. For the PhenoSense™ assay described herein, the reproducibility cut-off is 2.5-fold. For most protease inhibitors, the level of reduction in susceptibility required to overcome the achievable plasma 25 drug concentration is not well defined. However retrospective clinical studies using the 2.5-fold cutoff have suggested that this value is useful for predicting response to protease inhibitors, at least when used alone or in combination with reverse transcriptase inhibitors. 30 Recently, the use of dual protease inhibitor based regimens (typically involving co-dosing of an inhibitor with ritonavir or nelfinavir) has become popular, since the plasma drug levels can be significantly boosted due to

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inhibition of metabolic pathways. In cases such as these, it is likely that the clinically relevant fold-change cutoff will be higher, perhaps 10-fold. Future clinical studies will be required in order to accurately determine 5 the actual clinical cutoff value.

As used herein, what it is understood to mean "secondary mutations" in addition to the discussion on pages 7 and 8 of this specification, is that other mutations, not 10 currently recognized as resistance-associated, may also be defined as "secondary mutations" if they enhance the effects of primary mutations.

**Example 17**

15 **Predicting Response to Protease Inhibitors by Characterization of Amino Acid 82 of HIV-1 Protease.**

In one embodiment of this invention, changes in the amino acid at position 82 of the protease protein of HIV-1 are 20 evaluated using the following method comprising: (i) collecting a biological sample from an HIV-1 infected subject; (ii) evaluating whether the biological sample contains nucleic acid encoding HIV-1 protease having a valine to alanine (V82A), phenylalanine (V82F), serine 25 (V82S), threonine (V82T), or other amino acid substitution at codon 82 ("V82 mutations"); and (iii) determining susceptibility to protease inhibitors (PRI).

The biological sample comprises whole blood, blood 30 components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, cerebral spinal fluid (CSF), or other cell, tissue or body

fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after purification of virus particles from the biological 5 sample. Evaluating whether the amino acid at position 82 of the HIV-1 protease is mutated to alanine, phenylalanine, serine, threonine, or other amino acids, can be performed using various methods, such as direct characterization of the viral nucleic acid encoding 10 protease or direct characterization of the protease protein itself. Defining the amino acid at position 82 of protease can be performed by direct characterization of the protease protein by conventional or novel amino acid sequencing methodologies, epitope recognition by 15 antibodies or other specific binding proteins or compounds. Alternatively, the amino acid at position 82 of the HIV-1 protease protein can be defined by characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 20 nucleic acid can be performed using a variety of methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV protease at codon 82 can be determined by direct nucleic acid sequencing using 25 various primer extension-chain termination (Sanger, ABI/PE and Visible Genetics) or chain cleavage (Maxam and Gilbert) methodologies or more recently developed sequencing methods such as matrix assisted laser desorption-ionization time of flight (MALDI-TOF) or mass 30 spectrometry (Sequenom, Gene Trace Systems). Alternatively, the nucleic acid sequence encoding amino acid position 82 can be evaluated using a variety of probe hybridization methodologies, such as genechip

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hybridization sequencing (Affymetrix), line probe assay (LiPA; Murex), and differential hybridization (Chiron).

In a preferred embodiment of this invention, evaluation of 5 protease inhibitor susceptibility and of whether amino acid position 82 of HIV-1 protease was wild type or mutant was carried out using a phenotypic susceptibility assay or genotypic assay, respectively, using resistance test vector DNA prepared from the biological sample. In one 10 embodiment, plasma sample was collected, viral RNA was purified and an RT-PCR methodology was used to amplify a patient derived segment encoding the HIV-1 protease and reverse transcriptase regions. The amplified patient derived segments were then incorporated, via DNA ligation 15 and bacterial transformation, into an indicator gene viral vector thereby generating a resistance test vector. Resistance test vector DNA was isolated from the bacterial culture and the phenotypic susceptibility assay was carried out and analyzed as described in Example 1.

20 The nucleic acid (DNA) sequence of the patient derived HIV-1 protease and reverse transcriptase regions was determined using a fluorescence detection chain 25 termination cycle sequencing methodology (ABI/PE). The method was used to determine a consensus nucleic acid sequence representing the combination of sequences of the mixture of HIV-1 variants existing in the subject sample (representing the quasispecies), and to determine the nucleic acid sequences of individual variants. Genotypes 30 are analyzed as lists of amino acid differences between virus in the patient sample and a reference laboratory strain of HIV-1, NL4-3. Genotypes and corresponding phenotypes (fold-change in IC50 values) are entered in a

5        relational database linking these two results with patient information. Large datasets can then be assembled from patient virus samples sharing particular characteristics, such as the presence of any given mutation or reduced susceptibility to any drug or combination of drugs.

**(a)    Protease inhibitor susceptibility of viruses containing mutations at amino acid 82 of HIV-1 Protease.**

10      Phenotypic susceptibility profiles of 270 patient virus samples that contained a mutation at position 82 (but not at positions 30 or 50, which are primary mutations associated with resistance to nelfinavir and amprenavir, respectively) were analyzed. According to most published 15 guidelines, such viruses are expected to be resistant to ritonavir, nelfinavir, indinavir, and saquinavir. However, only 61.7% of these samples displayed reduced susceptibility to saquinavir using a 2.5-fold threshold (Table 13), while 31.2% and 40.0% displayed reduced 20 susceptibility to saquinavir and indinavir, respectively, using a 10-fold threshold (Table 14). Thus, there was poor correlation between the presence of mutations at position 82 and saquinavir or indinavir susceptibility.

25      **(b)    Indinavir susceptibility (fold change threshold 10) of viruses containing combinations of mutations at amino acid 82 and one secondary mutation in HIV-1 Protease.**

30      To explore the possibility that indinavir resistance (fold change in IC50 > 10-fold) in viruses containing mutations at position 82 requires the presence of other specific mutations, decreased indinavir susceptibility (fold-change in IC50 greater than 10) in viruses containing V82

mutations was correlated with the presence of mutations at other positions. This analysis revealed several positions (most strongly 73, 55, 48, 20, 43, 53, and 90) that decreased indinavir susceptibility significantly in combination with V82 mutations, compared to when these other mutations were absent (see Table 15). The presence of a mutation at position 13 significantly decreased the proportion of samples that had reduced indinavir susceptibility (45.9% vs. 62.2%; Table 15). In other words, the absence of a mutation at position 13 was correlated with decreased susceptibility to indinavir.

(c) Saquinavir susceptibility (fold change threshold 2.5) of viruses containing combinations of mutations at amino acid 82 and one secondary mutation in HIV-1 Protease.

To explore the possibility that saquinavir resistance in viruses containing mutations at position 82 requires the presence of other specific mutations, decreased saquinavir susceptibility (fold-change in IC50 greater than 2.5-fold) in viruses containing V82 mutations was correlated with the presence of mutations at other positions. This analysis revealed that several positions (most strongly 84, 48, 23, 73, 53, 33, 74, 20, and 90) were associated with reduced saquinavir susceptibility (See Table 16). The combination of mutations at position 82 with a mutation at position 32 or 39 significantly decreased the proportion of samples that had reduced saquinavir susceptibility (Table 16). In other words, the absence of a mutation at position 32 or 39 was correlated with decreased susceptibility to indinavir.

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(d) Saquinavir susceptibility (fold change threshold 10) of viruses containing combinations of mutations at amino acid 82 and one secondary mutation in HIV-1 Protease.

5 To explore the possibility that saquinavir resistance in viruses containing mutations at position 82 requires the presence of other specific mutations, decreased saquinavir susceptibility (fold-change in IC50 greater than 10 fold) in viruses containing V82 mutations was correlated with the presence of mutations at other positions. This 10 analysis revealed that several positions (most strongly 48, 23, 84, 53, 74, 20, 60, 33, 36, 35, and 90) were associated with reduced saquinavir susceptibility (See Table 17). The combination of mutations at position 82 15 with a mutation at position 32 or 46 significantly decreased the proportion of samples that had reduced saquinavir susceptibility (Table 17). In other words, the absence of a mutation at position 32 or 46 was correlated with decreased susceptibility to indinavir.

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**Example 18**

**Predicting Response to Protease Inhibitors by Characterization of Amino Acid 90 of HIV-1 Protease.**

25 In one embodiment of this invention, changes in the amino acid at position 90 of the protease protein of HIV-1 are evaluated using the following method comprising: (i) collecting a biological sample from an HIV-1 infected subject; (ii) evaluating whether the biological sample 30 contains nucleic acid encoding HIV-1 protease having a leucine to methionine (L90M) substitution at codon 90; and (iii) determining susceptibility to protease inhibitors (PRI).

The biological sample comprises whole blood, blood components including peripheral mononuclear cells (PBMC), serum, plasma (prepared using various anticoagulants such as EDTA, acid citrate-dextrose, heparin), tissue biopsies, 5 cerebral spinal fluid (CSF), or other cell, tissue or body fluids. In another embodiment, the HIV-1 nucleic acid (genomic RNA) or reverse transcriptase protein can be isolated directly from the biological sample or after purification of virus particles from the biological 10 sample. Evaluating whether the amino acid at position 90 of the HIV-1 protease is mutated to methionine, can be performed using various methods, such as direct characterization of the viral nucleic acid encoding protease or direct characterization of the protease 15 protein itself. Defining the amino acid at position 90 of protease can be performed by direct characterization of the protease protein by conventional or novel amino acid sequencing methodologies, epitope recognition by antibodies or other specific binding proteins or compounds. Alternatively, the amino acid at position 90 20 of the HIV-1 protease protein can be defined by characterizing amplified copies of HIV-1 nucleic acid encoding the protease protein. Amplification of the HIV-1 nucleic acid can be performed using a variety of 25 methodologies including reverse transcription-polymerase chain reaction (RT-PCR), NASBA, SDA, RCR, or 3SR. The nucleic acid sequence encoding HIV protease at codon 90 can be determined by direct nucleic acid sequencing using various primer extension-chain termination (Sanger, ABI/PE 30 and Visible Genetics) or chain cleavage (Maxam and Gilbert) methodologies or more recently developed sequencing methods such as matrix assisted laser desorption-ionization time of flight (MALDI-TOF) or mass

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spectrometry (Sequenom, Gene Trace Systems). Alternatively, the nucleic acid sequence encoding amino acid position 90 can be evaluated using a variety of probe hybridization methodologies, such as genechip hybridization sequencing (Affymetrix), line probe assay (LiPA; Murex), and differential hybridization (Chiron).

5 In a preferred embodiment of this invention, evaluation of protease inhibitor susceptibility and of whether amino acid position 90 of HIV-1 protease was wild type or methionine, was carried out using a phenotypic susceptibility assay or genotypic assay, respectively, using resistance test vector DNA prepared from the biological sample. In one embodiment, plasma sample was 10 collected, viral RNA was purified and an RT-PCR methodology was used to amplify a patient derived segment encoding the HIV-1 protease and reverse transcriptase regions. The amplified patient derived segments were then incorporated, via DNA ligation and bacterial 15 transformation, into an indicator gene viral vector thereby generating a resistance test vector. Resistance test vector DNA was isolated from the bacterial culture and the phenotypic susceptibility assay was carried out and analyzed as described in Example 1. The nucleic acid 20 (DNA) sequence of the patient derived HIV-1 protease and reverse transcriptase regions was determined using a fluorescence detection chain termination cycle sequencing methodology (ABI/PE). The method was used to determine a consensus nucleic acid sequence representing the 25 combination of sequences of the mixture of HIV-1 variants existing in the subject sample (representing the quasispecies), and to determine the nucleic acid sequences 30 of individual variants. Genotypes are analyzed as lists of

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amino acid differences between virus in the patient sample and a reference laboratory strain of HIV-1, NL4-3. Genotypes and corresponding phenotypes (fold-change in IC50 values) are entered in a relational database linking 5 these two results with patient information. Large datasets can then be assembled from patient virus samples sharing particular characteristics, such as the presence of any given mutation or reduced susceptibility to any drug or combination of drugs.

10

**(a) Protease inhibitor susceptibility of viruses containing mutations at amino acid 90 of HIV-1 Protease.**

15 Phenotypic susceptibility profiles of 333 patient virus samples which contained a mutation at position 90 (L90M) but not at positions 30 or 50, which are primary mutations associated with resistance to nelfinavir and amprenavir, respectively) were analyzed. According to most published guidelines, such viruses are expected to be resistant to 20 ritonavir, nelfinavir, indinavir, and saquinavir. However, only 79.3% and 84.7% of these samples displayed reduced susceptibility to saquinavir and indinavir, respectively, using a 2.5-fold threshold (Table 13), while 43.5% and 53.8% displayed reduced susceptibility to 25 saquinavir and indinavir, respectively, using a 10-fold threshold (Table 14). Thus, there was poor correlation between the presence of mutations at position 90 and saquinavir or indinavir susceptibility.

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**(b) Indinavir susceptibility (fold change threshold 2.5) of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.**

5 To explore the possibility that indinavir resistance in viruses containing a mutation at position 90 requires the presence of other specific mutations, decreased indinavir susceptibility (fold-change in IC50 greater than 2.5) in viruses containing L90M was correlated with the presence 10 of mutations at other positions. This analysis revealed several other positions (most strongly 53, 95, 54, 84, 82 and 46) that decreased indinavir susceptibility significantly in combination with the L90M mutation, compared to when these other mutations were absent (see 15 Table 18). The presence of a mutation at position 13 or 74 significantly decreased the proportion of samples that had reduced indinavir susceptibility (Table 18). In other words, the absence of mutations at position 13 or 74 was correlated with decreased susceptibility to indinavir.

20 **(c) Indinavir susceptibility (fold change threshold 10) of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.**

25 To explore the possibility that indinavir resistance in viruses containing a mutation at position 90 requires the presence of other specific mutations, decreased indinavir susceptibility (fold-change in IC50 greater than 10) in viruses containing L90M was correlated with the presence 30 of mutations at other positions. This analysis revealed several secondary positions (most strongly 95, 55, 54, 82, 85, 84, 20, 72, and 62) that decreased indinavir susceptibility significantly in combination with the L90M

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mutation, compared to when these other mutations were absent (see Table 19). The presence of a mutation at position 74 significantly decreased the proportion of samples that had reduced indinavir susceptibility (27.5% vs. 57.3%; Table 19). In other words, the absence of a mutation at position 74 was correlated with decreased susceptibility to indinavir.

10 **(d) Saquinavir susceptibility (fold change threshold 2.5) of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.**

15 To explore the possibility that saquinavir resistance in viruses containing a mutation at position 90 requires the presence of other specific mutations, decreased saquinavir susceptibility (fold-change in IC50 greater than 2.5) in viruses containing L90M was correlated with the presence of mutations at other positions. This analysis revealed several other positions (most strongly 53, 66, 84, 54, 48, 20 33, 73, 20, and 71) that decreased saquinavir susceptibility significantly in combination with the L90M mutation, compared to when these other mutations were absent (see Table 20). The presence of a mutation at position 64 or 93 significantly decreased the proportion of samples that had reduced saquinavir susceptibility (Table 20). In other words, the absence of a mutation at position 64 or 93 was correlated with decreased susceptibility to saquinavir.

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**(e) Saquinavir susceptibility (fold change threshold 10) of viruses containing combinations of mutations at amino acid 90 and one secondary mutation in HIV-1 Protease.**

5 To explore the possibility that saquinavir resistance in viruses containing a mutation at position 90 requires the presence of other specific mutations, decreased saquinavir susceptibility (fold-change in IC50 greater than 10) in viruses containing L90M was correlated with the presence 10 of mutations at other positions. This analysis revealed several other positions (most strongly 84, 53, 48, 23, 58, 20, 36, and 54) that decreased saquinavir susceptibility significantly in combination with the L90M mutation, compared to when these other mutations were absent (see 15 Table 21). The presence of a mutation at position 64, 77 or 93 significantly decreased the proportion of samples that had reduced saquinavir susceptibility (Table 21). In other words, the absence of a mutation at position 64, 77 or 93 was correlated with decreased susceptibility to 20 saquinavir.

**(f) Saquinavir susceptibility (fold change threshold 2.5) of viruses containing combinations of mutations at amino acid 90 and many secondary mutations in HIV-1 Protease.**

25 To explore the possibility that saquinavir resistance in viruses containing mutations at position 90 requires the presence of some defined number of other mutations, decreased saquinavir susceptibility (fold-change in IC50 30 greater than 2.5) in viruses containing L90M was correlated with the number of mutations at secondary positions. The following positions were considered: 10, 20, 52, 53, 54, 66, 71, 73, and 84; positions 53 and 84

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were weighted twice, yielding a saquinavir resistance-associated mutation count. This analysis revealed that 100% of samples with L90M and a mutation count of at least 5 had reduced saquinavir susceptibility (See Table 5 22). Combination with 3 or 4 other secondary mutations also significantly increased the proportion of samples that had reduced saquinavir susceptibility (85.7% and 97.3%, respectively; see Table 22).

10 **Table 13. PRI Susceptibility of Viruses with Mutations at 82 and/or 90 (fold change threshold > 2.5).**

Drug	Percent of viruses with indicated primary mutation(s) with reduced susceptibility (fold change in IC <sub>50</sub> > 2.5)	
	V82 mutations	L90M
Amprenavir	60.0	60.4
Indinavir	92.2	84.7
Nelfinavir	94.4	97.0
Ritonavir	97.8	93.4
Saquinavir	61.7	79.3

20

Table 14. PRI Susceptibility of Viruses with Mutations at 82 and/or 90 (fold change threshold > 10).

25

Drug	Percent of viruses with indicated primary mutation(s) with reduced susceptibility (fold change in IC <sub>50</sub> > 10)	
	V82 mutations	L90M
Amprenavir	10.4	12.9
Indinavir	60.0	53.8
Nelfinavir	68.9	74.5
Ritonavir	89.3	66.1
Saquinavir	31.2	43.5

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Table 15. Correlation Between V82 mutations, Secondary Mutations, and Indinavir Susceptibility (fold change threshold > 10).

	<u>position + or -</u>	<u>n</u>	<u>mt % &gt;10</u>	<u>wt %&gt;10</u>	<u>p value</u>
5	73	22	90.9	57.3	0.0011
	55	25	80.0	58.0	0.0238
	48	35	77.1	57.4	0.0188
	20	77	76.6	53.4	<0.001
	43	34	76.5	57.6	0.0258
	53	33	75.8	57.8	0.0349
	90	135	74.1	45.9	<0.001
	72	56	73.2	56.5	0.0160
	35	91	72.5	53.6	0.0019
	54	188	71.3	34.1	<0.001
10	71	184	70.7	37.2	<0.001
	36	99	69.7	54.4	0.0091
	10	224	66.1	30.4	<0.001
	82	270	60.0		
	13	37	45.9	62.2	0.0458
20					

Table 16. Correlation Between V82 mutations, Secondary Mutations, and Saquinavir Susceptibility (fold change threshold > 2.5)

	position	+	or	-	n	mt	% >2.5	wt	% >2.5	p value
	84	+			36	100.0		55.8		<0.001
	48	+			35	97.1		56.4		<0.001
	23	+			11	90.9		60.5		0.0358
30	73	+			22	90.9		59.1		0.0018
	53	+			33	87.9		58.1		<0.001
	33	+			24	87.5		59.2		0.0041
	74	+			25	84.0		59.4		0.0113
	20	+			77	83.1		53.1		<0.001
35	90	+			135	82.2		41.0		<0.001
	43	+			34	79.4		59.1		0.0162
	36	+	.		99	75.8		53.5		<0.001
	41	+			79	74.7		56.3		0.0032
	54	+			187	74.3		32.9		<0.001
40	71	+			183	74.3		34.9		<0.001
	35	+			91	73.6		55.6		0.0028
	10	+			223	69.5		23.9		<0.001
	82				269	61.7				
	32	-			24	37.5		64.1		0.0106
45	39	-			4	0.0		62.6		0.0207

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Table 17. Correlation Between V82 mutations, Secondary Mutations, and Saquinavir Susceptibility (fold change threshold > 10)

5	position + or -	n	mt % >10	wt %>10	p value
48	+	35	82.9	23.5	<0.001
23	+	11	81.8	29.1	<0.001
84	+	36	72.2	24.9	<0.001
53	+	33	69.7	25.8	<0.001
10	74	25	56.0	28.7	0.0062
	20	77	55.8	21.4	<0.001
	60	30	50.0	28.9	0.0181
	33	24	50.0	29.4	0.0352
	36	99	47.5	21.8	<0.001
15	35	91	44.0	24.7	0.0011
	90	135	43.0	19.4	<0.001
	41	79	41.8	26.8	0.0126
	62	119	41.2	23.3	0.0013
	54	187	39.0	13.4	<0.001
20	71	183	37.7	17.4	<0.001
	10	223	35.0	13.0	0.0019
	82	269	31.2		
	46	156	26.3	38.1	0.0275
	32	24	12.5	33.1	0.0268

25

Table 18. Correlation Between L90M, Secondary Mutations, and Indinavir Susceptibility (fold change threshold > 2.5).

30	position+ or -	n	mt % >2.5	wt %>2.5	p value
35	53	29	100.0	83.2	0.0064
	95	23	100.0	83.5	0.0189
	54	129	98.4	76.0	<0.001
	84	104	97.1	79.0	<0.001
	82	135	94.1	78.3	<0.001
	46	164	93.3	76.3	<0.001
	73	117	92.3	80.6	0.0027
	71	233	91.4	69.0	<0.001
40	20	115	91.3	81.2	0.0095
	10	255	90.2	66.7	<0.001
	63	325	85.5	50.0	0.0214
	90	333	84.7		
	13	77	76.6	87.1	0.0226
45	74	40	67.5	87.0	0.0028

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Table 19. Correlation Between L90M, Secondary Mutations,  
and Indinavir Susceptibility (fold change threshold > 10).

	position	+	or -	n	mt % >10	wt %>10	p value
5	95	+		23	82.6	51.6	0.0030
	55	+		22	81.8	51.8	0.0048
	54	+		129	81.4	36.3	<0.001
	82	+		135	74.1	39.9	<0.001
	85	+		23	73.9	52.3	0.0346
10	84	+		104	70.2	46.3	<0.001
	20	+		115	66.1	47.2	0.0103
	72	+		87	64.4	50.0	0.0141
	62	+		154	63.6	45.3	<0.001
	46	+		164	63.4	44.4	<0.001
15	36	+		114	63.2	48.9	0.0088
	10	+		255	63.1	23.1	<0.001
	71	+		233	60.9	37.0	<0.001
	90			333	53.8		
	74	-		40	27.5	57.3	<0.001

20

Table 20. Correlation Between L90M, Secondary Mutations,  
and Saquinavir Susceptibility (fold change threshold >  
2.5).

	position	+	or -	n	mt % >2.5	wt %>2.5	p value
25	53	+		29	100.0	77.3	<0.001
	66	+		13	100.0	78.4	0.0459
	84	+		104	98.1	70.7	<0.001
	54	+		129	96.9	68.1	<0.001
	48	+		22	95.5	78.1	0.0362
30	33	+		37	94.6	77.4	0.0076
	73	+		117	89.7	73.6	<0.001
	20	+		115	89.6	73.9	<0.001
	71	+		233	88.4	58.0	<0.001
	36	+		114	87.7	74.9	0.0038
35	10	+		255	86.3	56.4	<0.001
	37	+		104	85.6	76.4	0.0365
	63	+		325	80.3	37.5	0.0112
	90			333	79.3		
	93	-		187	74.3	85.6	0.0080
40	64	-		66	63.6	83.1	<0.001

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**Table 21. Correlation Between L90M, Secondary Mutations, and Saquinavir Susceptibility (fold change threshold > 10).**

	position	+	or -	n	mt % >10	wt %>10	p value
5	84	+		104	84.6	24.9	<0.001
	53	+		29	82.8	39.8	<0.001
	48	+		22	81.8	40.8	<0.001
	23	+		12	75.0	42.4	0.0260
10	58	+		30	63.3	41.6	0.0182
	20	+		115	61.7	33.9	<0.001
	36	+		114	61.4	34.2	<0.001
	54	+		129	60.5	32.8	<0.001
15	35	+		109	53.2	38.8	0.0091
	73	+		117	51.3	39.4	0.0240
	10	+		255	50.6	20.5	<0.001
	71	+		233	49.8	29.0	<0.001
	62	+		154	49.4	38.5	0.0306
	90			333	43.5		
20	93	-		187	38.0	50.7	0.0135
	77	-		139	35.3	49.5	0.0066
	64	-		66	33.3	46.1	0.0409

**Table 22. Association Between Saquinavir Susceptibility, L90M, and Number of Resistance Associated Mutations.**

	Number of secondary mutations	n	% with SQV FC > 2.5	Mean SQV fold change
30	0	17	23.5	2.4
	1	40	25.0	2.4
	2	49	69.4	5.4
	3	63	85.7	10.0
	4	74	97.3	36.6
	5	34	100	50.3
35	6 or more	56	100	94.2

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Tables 23-27 show results as indicated using the above procedures as described in Examples 17 and 18.

5 **Table 23. Correlation Between L90M, Secondary Mutations, and Amprenavir Susceptibility (fold change threshold > 2.5).**

Amprenavir								
	position	+	or	-	n	mt % >2.5	wt % >2.5	p value
10	89	+		-	11	90.9	59.3	0.0298
	53	+		-	29	89.7	57.6	<0.001
	84	+		-	104	86.5	48.5	<0.001
	33	+		-	37	83.8	57.4	0.0012
15	92	+		-	24	83.3	58.6	0.0120
	95	+		-	23	82.6	58.7	0.0174
	54	+		-	129	80.6	47.5	<0.001
	58	+		-	30	76.7	58.7	0.0400
	46	+		-	164	75.0	46.2	<0.001
20	82	+		-	135	70.4	53.5	0.0014
	36	+		-	114	70.2	55.3	0.0055
	10	+		-	255	69.4	30.8	<0.001
	62	+		-	154	66.2	55.3	0.0272
	90				333	60.4		
25	74	-			40	45.0	62.5	0.0269
	15	-			53	43.4	63.6	0.0050

30 **Table 24. Correlation Between L90M, Secondary Mutations, and Amprenavir Susceptibility (fold change threshold > 10).**

Amprenavir								
	position	+	or	-	n	% >10	wt % >10	p value
35	47	+		-	5	80.0	11.9	0.0011
	33	+		-	37	48.6	8.4	<0.001
	66	+		-	13	38.5	11.9	0.0166
40	32	+		-	16	37.5	11.7	0.0097
	55	+		-	22	31.8	11.6	0.0140
	53	+		-	29	27.6	11.5	0.0213
	54	+		-	129	24.0	5.9	<0.001
45	84	+		-	104	22.1	8.7	0.0010
	13	+		-	77	19.5	10.9	0.0424
	46	+		-	164	17.7	8.3	0.0080
	10	+		-	255	16.1	2.6	<0.001
	90				333	12.9		
	69	-			37	2.7	14.2	0.0316

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Table 25. Correlation Between V82, Secondary Mutations, and Indinavir Susceptibility (fold change threshold > 2.5)

Indinavir								
	position	+	or	-	n	mt % >2.5	wt % >2.5	p value
5	84	+		-	37	100.0	91.0	0.0397
	20	+		-	77	98.7	89.6	0.0064
	72	+		-	56	98.2	90.7	0.0432
	54	+		-	188	97.3	80.5	<0.001
	71	+		-	184	97.3	81.4	<0.001
	46	+		-	157	95.5	87.6	0.0155
	93	+		-	133	95.5	89.1	0.0391
	10	+		-	224	94.6	80.4	0.0034
	82			-	270	92.2		
	37	-		-	108	88.0	95.1	0.0297
10	64	-		-	56	85.7	93.9	0.0451
	13	-		-	37	70.3	95.7	<0.001
	45	-		-	12	58.3	93.8	<0.001

20

Table 26. Correlation Between V82, Secondary Mutations, and Amprenavir Susceptibility (fold change threshold > 2.5)

25

Amprenavir								
	position	+	or	-	n	mt % >2.5	wt % >2.5	p value
30	33	+		-	24	95.8	56.5	<0.001
	23	+		-	12	91.7	58.5	0.0176
	84	+		-	37	86.5	55.8	<0.001
	32	+		-	24	83.3	57.7	0.0104
	53	+		-	33	81.8	57.0	0.0042
	90	+		-	135	70.4	49.6	<0.001
35	37	+		-	108	66.7	55.6	0.0442
	71	+		-	184	66.3	46.5	0.0016
	46	+		-	157	65.6	52.2	0.0184
	10	+		-	224	65.2	34.8	<0.001
	54	+		-	188	63.8	51.2	0.0356
40	82			-	270	60.0		
	61	-		-	21	38.1	61.8	0.0297

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Table 27. Correlation Between V82, Secondary Mutations, and Amprenavir Susceptibility (fold change threshold > 10).

Amprenavir		position	or	-	n	mt %	>10	wt %>10	p value
+	-								
5	33	+		-	24	50.0		6.5	<0.001
	11	+		-	8	37.5		9.5	0.0394
	84	+		-	37	35.1		6.4	<0.001
	32	+		-	24	25.0		8.9	0.0258
	10	+		-	30	23.3		8.8	0.0229
	60	+		-	33	21.2		8.9	0.0382
	53	+		-	135	14.8		5.9	0.0133
	90	+		-	157	14.6		4.4	0.0046
	46	+		-	184	13.0		4.7	0.0243
	15	+		-	224	12.5		0.0	0.0039
	82				270	10.4			

20 In Tables 13-27, the first column lists the various codon positions for HIV-1 protease for the secondary mutations and the primary mutation at codon 82 or 90.

25 The second column represents a positive (+) or negative (-) correlation between the change in resistance from the number of wild-type reference samples to those samples having the secondary mutation.

30 The fourth column, designates "mt %", as the percentage of samples having the secondary mutation and showing the indicated fold resistance to the specified protease inhibitor, (i.e., > 10 fold or > 2.5 fold).

35 The fifth column, designates "wt %", as the percentage of wild-type reference samples showing the indicated fold resistance, (i.e., > 10 fold or > 2.5 fold) to the specified protease inhibitor.

40 The sixth column represents the statistical P value for a correlation.

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5 The following list of mutations represents, by example, secondary mutations from a database for selected patient samples used to establish the above data in Tables 13-27. The mutations listed show the wild type reference amino acid and the possible various mutations for the substituted amino acid at the designated codon position for HIV-1 protease.

10 L10F/I/R/V, I13V, K20I/M/R/T/V  
L23I, V32I, L33F/I/V  
E35/D/N/G, M36I/L/T/V, N37C/D/E/G/H/S/T  
P39A/Q/S/T, R41K/W/S, K43R/T  
K45R, M46I/L/V, G48M/S/V  
15 S53L/Y, I54A/L/M/S/T/V, K55N/R  
Q58E, D60E, I62/V/M,  
L63A/C/D/S/H/I/N/P/Q/R/S/T/V/Y  
I64L/M/V, I66F/L/T/V, A71I/L/T/V  
I72A/E/K/L/M/R/T/V, G73A/C/S/T, T74A/K/P/S  
20 V77I/T, V82A/F/S/T, I84A/M/V, I85V  
L90M, I93L/M, C95F

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Detailed Description of the Invention (continued)

In another embodiment, the present invention provides a method for determining whether an HIV virus obtained from a patient infected with HIV is resistant to IDV, LPV, NFV and RTV which comprises determining whether a mutation at position 30 from D to N exists in the HIV protease obtained from the patient, wherein the presence of the mutation indicates that the virus is resistant to IDV, LPV, NFV and RTV.

In another embodiment, the present invention provides a method for determining whether an HIV virus obtained from a patient infected with HIV is resistant to IDV, LPV, NFV or RTV which comprises determining whether the virus is resistant to any one of IDV, LPV, NFV or RTV, wherein a determination that the virus is resistant to any one of IDV, LPV, NFV or RTV is indicative of the virus being resistant to IDV, LPV, NFV and RTV.

In a further embodiment, the present invention provides a method for determining cross resistance of an HIV virus to RTV and SQV which comprises determining (i) whether position 30 of the HIV protease is D, and (ii) whether the virus is resistant to NFV, wherein a mutation from D to N at position 30 of HIV protease and resistance of the virus to NFV are indicative of cross resistance to IDV and SQV.

In yet another embodiment the invention provides a method for determining whether an HIV virus obtained from a patient infected with HIV is resistant to LPV and IND which comprises determining whether position 50 of the HIV protease of the virus is I or V, wherein the determination that position 50 is V is indicative of the virus being resistant to LPV and IND. These and other embodiments of the invention are shown and described with reference to the accompanying Figures 6-28 in view of the specification contained herein.

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5      What is claimed is:

1. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
  - 10            (a) collecting a plasma sample from the HIV-infected patient;
  - (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 88; and
  - 15            (c) determining increased susceptibility to amprenavir.
2. The method of claim 1, wherein the mutation at codon 88 codes for a serine (S).
- 20            3. The method of claim 1, wherein the HIV-infected patient is being treated with an antiretroviral agent.
- 25            4. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:
  - 25            (a) collecting a plasma sample from the HIV-infected patient;
  - (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 88 and additional mutations at codons 63 and/or 77 or a combination thereof; and
  - 30            (c) determining decreased susceptibility to nelfinavir and indinavir and increased susceptibility to amprenavir.
- 35            5. The method of claim 4, wherein the mutation at codon 63 codes for a proline (P) or a glutamine (Q) and the mutation at codon 77 codes for an isoleucine (I).

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5

6. The method of claim 4, wherein the HIV-infected patient is being treated with an antiretroviral agent.

10

7. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

15

(a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 88 and additional mutations at codons 63, 77 and/or 46 or a combination thereof; and

20

(c) determining decreased susceptibility to nelfinavir and indinavir and increased susceptibility to amprenavir.

25

8. The method of claim 7, wherein the mutation at codon 63 codes for a proline (P) or a glutamine (Q), the mutation at codon 77 codes for an isoleucine (I). and the mutation at codon 46 codes for a leucine (L) or an isoleucine (I).

30

9. The method of claim 7, wherein the HIV-infected patient is being treated with an antiretroviral agent.

35

10. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 88 and additional mutations at codons 63, 77, 46, 10, 20, and/or 36 or a

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5 combination thereof; and

(c) determining decreased susceptibility to nelfinavir and indinavir and increased susceptibility to amprenavir.

10 11. The method of claim 10, wherein the mutation at codon  
63 codes for a proline (P) or a glutamine (Q), the  
mutation at codon 77 codes for an isoleucine (I), the  
mutation at codon 46 codes for a leucine (L) or an  
isoleucine (I), the mutation at codon 10 codes for a  
15 isoleucine (I) or a phenylalanine (F), the mutation at  
20 codes for a threonine (T) or a methionine (M) or an  
arginine (R), and the mutation at 36 codes for an  
isoleucine (I) or a valine (V).

20 12. The method of claim 10, wherein the HIV-infected  
patient is being treated with an antiretroviral agent.

13. A method for evaluating the biological effectiveness of  
a candidate HIV antiretroviral drug compound  
comprising:

- (a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 88 and an indicator gene into a host cell;

30 (b) culturing the host cell from step (a); -  
(c) measuring the indicator in a target host cell; and  
(d) comparing the measurement of the indicator from  
step (c) with the measurement of the indicator  
measured when steps (a) - (c) are carried out in  
the absence of the candidate antiretroviral drug  
compound;

35

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

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5 14. A method for evaluating the biological effectiveness of  
a candidate HIV antiretroviral drug compound  
comprising:

10 (a) introducing a resistance test vector comprising a  
patient-derived segment further comprising a  
mutation at codon 88 and mutation(s) at codons 63  
and/or 77 or a combination thereof and an  
indicator gene into a host cell;  
(b) culturing the host cell from step (a);  
(c) measuring the indicator in a target host cell; and  
15 (d) comparing the measurement of the indicator from  
step (c) with the measurement of the indicator  
measured when steps (a) - (c) are carried out in  
the absence of the candidate antiretroviral drug  
20 compound;

wherein a test concentration of the candidate  
antiretroviral drug compound is present at steps (a) -  
(c); at steps (b) - (c); or at step (c).

25 15. A method for evaluating the biological effectiveness of  
a candidate HIV antiretroviral drug compound  
comprising:

30 (a) introducing a resistance test vector comprising a  
patient-derived segment further comprising a  
mutation at codon 88 and mutation(s) at codons 63,  
77, and/or 46 or a combination thereof and an  
indicator gene into a host cell;  
(b) culturing the host cell from step (a);  
35 (c) measuring the indicator in a target host cell; and  
(d) comparing the measurement of the indicator from  
step (c) with the measurement of the indicator  
measured when steps (a) - (c) are carried out in  
the absence of the candidate antiretroviral drug  
40 compound;

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5 wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

10 16. A method for evaluating the biological effectiveness of a candidate HIV antiretroviral drug compound comprising:

15 (a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 88 and mutation(s) at codons 63, 77, 46, 10, 20, and/or 36 or a combination thereof and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

(d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

20 wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

25 17. A resistance test vector comprising an HIV — patient-derived segment further comprising protease having a mutation at codon 88 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient derived segment.

30 18. The resistance test vector of claim 17, wherein the patient-derived segment having a mutation at codon 88 further comprises mutations at codons 63 and 77 or a combination thereof.

35 19. The resistance test vector of claim 17, wherein the patient-derived segment having a mutation at codon 88 further comprises mutations at codons 63, 77 and/or 46

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5 or a combination thereof.

20. The resistance test vector of claim 17, wherein the patient-derived segment having a mutation at codon 88 further comprises mutations at codons 63, 77, 46, 10, 10 20 and/or 36 or a combination thereof.

21. A method for evaluating the viral fitness of a patient's virus comprising:

15 (a) introducing a resistance test vector comprising a patient-derived segment from a patient's virus and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

20 (c) measuring the luciferase activity in a target host cell in the absence of any antiretroviral drug; and

25 (d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a)-(c) are carried out for a reference control in the absence of any antiretroviral drug;

wherein a reduction in the luciferase activity measured in step (c) as compared to step (d) indicates a reduction in viral fitness.

30 22. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a plasma sample from the HIV-infected patient;

35 (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and secondary positions; and

(c) determining changes in susceptibility to ritonavir, nelfinavir, indinavir, saquinavir and amprenavir.

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5        23. The method of claim 22, wherein the mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

10      24. The method of claim 22, wherein the HIV-infected patient is being treated with an antiretroviral agent.

20      25. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

15        (a) collecting a plasma sample from the HIV-infected patient;

            (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and an additional mutation at codon 24; and

20        (c) determining decreased susceptibility to indinavir.

25      26. The method of claim 25, wherein the mutation at codon 24 codes for an isoleucine (I).

30      27. The method of claim 25, wherein the HIV-infected patient is being treated with an antiretroviral agent.

35      28. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

            (a) collecting a plasma sample from the HIV-infected patient;

            (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and an additional mutation at codon 71; and

            (c) determining decreased susceptibility to indinavir.

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5 29. The method of claim 28, wherein the mutation at codon 71 codes for an amino acid selected from the group consisting of a threonine, (T) valine, (V) leucine (L) and isoleucine (I).

10 30. The method of claim 28, wherein the HIV-infected patient is being treated with an antiretroviral agent.

15 31. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

20 (a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and additional mutations at codons selected from the group consisting of codon 54, 46, 10, 63, and a combination thereof; and

25 (c) determining decreased susceptibility to indinavir.

30 32. The method of claim 31, wherein the mutation at codon 54 codes for an amino acid selected from the group consisting of a valine (V), alanine (A), leucine (L) and threonine (T), the mutation at codon 46 codes for an amino acid selected from the group consisting of a leucine (L), isoleucine (I) and valine (V), the mutation at codon 10 codes for an amino acid selected from the group consisting of an isoleucine (I), valine (V), phenylalanine (F), and arginine (R), and the mutation at codon 63 codes for an amino acid selected from the group consisting of proline (P), alanine (A), serine (S), threonine (T), glutamine (Q), , cysteine (C), and valine (V).

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5 33. The method of claim 31, wherein the HIV-infected patient is being treated with an antiretroviral agent.

10 34. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

15 (a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and an additional mutation at codon 20; and

(c) determining decreased susceptibility to saquinavir.

20 35. The method of claim 34, wherein the mutation at codon 20 codes for an amino acid selected from the group consisting of a methionine (M), threonine (T), isoleucine (I), and arginine (R).

25 36. The method of claim 34, wherein the HIV-infected patient is being treated with an antiretroviral agent.

30 37. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

35 (a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and an additional mutation at codon 36; and

(c) determining decreased susceptibility to saquinavir.

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5 38. The method of claim 37, wherein the mutation at codon  
36 for an amino acid selected from the group consisting  
of a isoleucine (I), leucine (L), and valine (V).

10 39. The method of claim 37, wherein the HIV-infected  
patient is being treated with an antiretroviral  
agent.

15 40. A method of assessing the effectiveness of protease  
antiretroviral therapy of an HIV-infected patient  
comprising:  
20 (a) collecting a plasma sample from the HIV-infected  
patient;  
(b) evaluating whether the plasma sample contains  
nucleic acid encoding HIV protease having a  
mutation at codon 82 and additional mutations at  
codons 24, 71, 54, and/or 10 or a combination  
thereof; and  
(c) determining decreased susceptibility to saquinavir.

25 41. The method of claim 40, wherein the mutation at codon  
24 codes for an isoleucine (I), the mutation at codon  
71 codes for an amino acid selected from the group  
consisting of a threonine (T), valine (V), leucine (L),  
30 and isoleucine (I), the mutation at codon 54 codes for  
an amino acid selected from the group consisting of  
valine (V), alanine (A), leucine (L), and threonine  
(T), and the mutation at codon 10 codes for an amino  
acid selected from the group consisting of an  
isoleucine (I), valine (V), phenylalanine (F), and  
35 arginine (R).

42. The method of claim 40, wherein the HIV-infected  
patient is being treated with an antiretroviral  
agent.

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5        43. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

10        (a) collecting a plasma sample from the HIV-infected patient;

15        (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and the number of additional mutations at secondary positions; and

15        (c) determining decreased susceptibility to indinavir and saquinavir.

20        44. The method of claim 43, wherein the number of additional mutations at secondary positions is at least 3.

20        45. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

25        (ss) collecting a plasma sample from the HIV-infected patient;

25        (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and secondary mutations; and

30        (c) determining changes in susceptibility to ritonavir, nelfinavir, indinavir, saquinavir and amprenavir.

35        46. The method of claim 45, wherein the mutation at codon 90 codes for a methionine.

35        47. The method of claim 45, wherein the HIV-infected patient is being treated with an antiretroviral agent.

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5 48. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(d) collecting a plasma sample from the HIV-infected patient;

10 (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 73; and

(c) determining decreased susceptibility to indinavir.

15

49. The method of claim 48, wherein the mutation at codon 73 codes for an amino acid selected from the group consisting of a serine (S), threonine (T), and cysteine (C).

20

50. The method of claim 48, wherein the HIV-infected patient is being treated with an antiretroviral agent.

25

51. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

(d) collecting a plasma sample from the HIV-infected patient;

30 (b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 71; and

(c) determining decreased susceptibility to indinavir.

35

52. The method of claim 51, wherein the mutation at codon 71 codes for an amino acid selected from the group consisting of a threonine (T), valine (V), leucine (L), and isoleucine (I).

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5 53. The method of claim 51, wherein the HIV-infected patient is being treated with an antiretroviral agent.

10 54. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

15 (d) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 46; and

(c) determining decreased susceptibility to indinavir.

20 55. The method of claim 54, wherein the mutation at codon 46 codes for an amino acid selected from the group consisting of a leucine (L), isoleucine (I) and valine (V).

25 56. The method of claim 54, wherein the HIV-infected patient is being treated with an antiretroviral agent.

30 57. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

35 (d) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 73; and

(c) determining decreased susceptibility to saquinavir.

40 58. The method of claim 57, wherein the mutation at codon 73 codes for an amino acid selected from the group

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5 consisting of a serine (S), threonine (T), and cysteine (C).

10 59. The method of claim 57, wherein the HIV-infected patient is being treated with an antiretroviral agent.

15 60. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

20 (d) collecting a plasma sample from the HIV-infected patient;  
(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and an additional mutation at codon 71; and  
(c) determining decreased susceptibility to saquinavir.

25 61. The method of claim 60, wherein the mutation at codon 71 codes for an amino acid selected from the group consisting of a threonine (T), valine (V), leucine (L), and isoleucine (I).

30 62. The method of claim 60, wherein the HIV-infected patient is being treated with an antiretroviral agent.

63. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

35 (d) collecting a plasma sample from the HIV-infected patient;  
(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and additional mutations at codons 77 and 10; and

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5 (c) determining decreased susceptibility to saquinavir.

10 64. The method of claim 63, wherein the mutation at codon 77 codes for an amino acid selected from the group consisting of isoleucine (I) and threonine (T) and the mutation at codon 10 codes for an amino acid selected from the group consisting of isoleucine (I), valine (V), phenylalanine (F), and arginine (R).

15 65. The method of claim 63, wherein the HIV-infected patient is being treated with an antiretroviral agent.

20 66. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

25 (d) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codon 90 and the number of additional mutations at secondary positions; and

30 (c) determining decreased susceptibility to indinavir and saquinavir.

35 67. The method of claim 66, wherein the number of additional mutations at secondary positions is at least 3.

68. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:

40 (a) collecting a plasma sample from the HIV-infected patient;

(b) evaluating whether the plasma sample contains nucleic acid encoding HIV protease having a mutation at codons 82 and 90 and secondary mutations; and

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5 (c) determining changes in susceptibility to ritonavir, nelfinavir, indinavir, saquinavir and amprenavir.

10 69. The method of claim 68, wherein the mutation at codon 82 codes for an amino acid selected from the group consisting of alanine (A), phenylalanine (F), serine (S), and threonine (T) and the mutation at codon 90 codes for a methionine (M).

15 70. The method of claim 68, wherein the HIV-infected patient is being treated with an antiretroviral agent.

20 71. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

25 (a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 82 and additional mutations at one or more secondary positions and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

30 (d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

35 wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

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5 72. A method for evaluating the biological effectiveness of  
a candidate HIV protease antiretroviral drug compound  
comprising:

10 (a) introducing a resistance test vector comprising a  
patient-derived segment further comprising a  
mutation at codon 82 and secondary mutation(s) at  
codons 20, 24, 71, 54 and/or 10 or a combination  
thereof and an indicator gene into a host cell;  
(b) culturing the host cell from step (a);  
(c) measuring the indicator in a target host cell; and  
15 (d) comparing the measurement of the indicator from  
step (c) with the measurement of the indicator  
measured when steps (a) - (c) are carried out in  
the absence of the candidate antiretroviral drug  
compound;

20 wherein a test concentration of the candidate  
antiretroviral drug compound is present at steps (a) -  
(c); at steps (b) - (c); or at step (c).

25 73. A method for evaluating the biological effectiveness of  
a candidate HIV protease antiretroviral drug compound  
comprising:

30 (a) introducing a resistance test vector comprising a  
patient-derived segment further comprising a  
mutation at codon 90 and additional mutations at  
one or more secondary positions and an indicator  
gene into a host cell;  
(b) culturing the host cell from step (a);  
(c) measuring the indicator in a target host cell; and  
35 (d) comparing the measurement of the indicator from  
step (c) with the measurement of the indicator  
measured when steps (a) - (c) are carried out in  
the absence of the candidate antiretroviral drug  
compound;

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5 wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

10 74. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

15 (a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codon 90 and secondary mutation(s) at codons 73, 71, 10 and/or 46 or a combination thereof and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

20 (d) comparing the measurement of the indicator from step (c) with the measurement of the indicator measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

25 wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

30 75. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

35 (a) introducing a resistance test vector comprising a patient-derived segment further comprising a mutation at codons 82 and 90 and additional mutations at one or more secondary positions and an indicator gene into a host cell;

(b) culturing the host cell from step (a);

(c) measuring the indicator in a target host cell; and

40 (d) comparing the measurement of the indicator from step (c) with the measurement of the indicator

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5

measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

10

wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

15

76. A resistance test vector comprising an HIV patient-derived segment further comprising protease having a mutation at codon 82 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient derived segment.

20

77. The resistance test vector of claim 76, wherein the patient-derived segment having a mutation at codon 82 further comprises at least one secondary mutation at a codon selected from the group consisting of 20, 24, 71, 54, 10 and a combination thereof.

25

78. The resistance test vector of claim 76, wherein the patient-derived segment having a mutation at codon 90 further comprises at least one secondary mutation at a codon selected from the group consisting of 73, 71, 46, 10 and a combination thereof.

30

79. A method for determining replication capacity for a patient's virus comprising:

35

- (a) introducing a resistance test vector comprising a patient derived segment and an indicator gene into a host cell;
- (b) culturing the host cell from (a);
- (c) harvesting viral particles from step (b) and infecting target host cells;
- (d) measuring expression of the indicator gene in the target host cell, wherein the expression of the

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5 indicator gene is dependent upon the patient-derived segment;

(e) comparing the expression of the indicator gene from (d) with the expression of the indicator gene measured when steps (a) through (d) are carried

10 out in a control resistance test vector; and

(f) normalizing the expression of the indicator gene by measuring an amount of virus in step (c).

80. A method of assessing the effectiveness of protease  
15 antiretroviral therapy of an HIV-infected patient comprising:

(a) collecting a biological sample from the HIV-infected patient;

(b) evaluating whether the biological sample contains  
20 nucleic acid encoding HIV protease having a mutation at codon 82 or codon 90; and

(c) determining changes in susceptibility to protease inhibitors.

25 81. The method of claim 80, wherein step (c) determines changes in susceptibility to saquinavir.

82. The method of claim 80, wherein the mutation at codon  
30 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

83. The method of claim 82, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V).

35 84. The method of claim 80, wherein the mutation at codon 90 codes for methionine (M).

85. The method of claim 84, wherein the mutation at codon  
10 90 is a substitution of methionine (M) for leucine (L).

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5 86. A method for evaluating the biological effectiveness of a candidate HIV protease antiretroviral drug compound comprising:

0 (a) introducing a resistance test vector comprising a patient-derived segment having nucleic acid encoding HIV protease with a mutation at codon 82 or codon 90 and an indicator gene into a host cell;

.5 (b) culturing the host cell from step (a);

5 (c) measuring the indicator gene in a target host cell; and

10 (d) comparing the measurement of the indicator gene from step (c) with the measurement of the indicator gene measured when steps (a) - (c) are carried out in the absence of the candidate antiretroviral drug compound;

15 wherein a test concentration of the candidate antiretroviral drug compound is present at steps (a) - (c); at steps (b) - (c); or at step (c).

20 87. A resistance test vector comprising an HIV patient-derived segment, further comprising protease having a mutation at codon 82 or codon 90 and an indicator gene, wherein the expression of the indicator gene is dependent upon the patient-derived segment.

25 88. The resistance test vector of claim 87, wherein the patient-derived segment having a mutation at codon 82 codes for alanine (A), phenylalanine (F), serine (S), or threonine (T).

30 89. The resistance test vector of claim 88, wherein the patient-derived segment having a mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V).

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5 90. The resistance test vector of claim 87, wherein the patient-derived segment having a mutation at codon 90 codes for methionine (M).

10 91. The resistance test vector of claim 90, wherein the patient-derived segment having a mutation at codon 90 is a substitution of methionine (M) for leucine (L).

15 92. A method for determining replication capacity for a patient's virus comprising:

20 (a) introducing a resistance test vector comprising a patient-derived segment and an indicator gene into a host cell;

(b) culturing the host cell from (a);

(c) harvesting viral particles from step (b) and infecting target host cells;

(d) measuring expression of the indicator gene in the target host cell, wherein the expression of the indicator gene is dependent upon the patient-derived segment; and

25 (e) comparing the expression of the indicator gene from (d) with the expression of the indicator gene measured when steps (a) through (d) are carried out in a control resistance test vector.

30 93. The method of claim 92 further comprising the step of:

(f) normalizing the expression of the indicator gene by measuring an amount of virus in step (c).

35 94. The method of claim 92 wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having a mutation at codon 66.

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5 95. The method of claim 92 wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having a mutation at codon 154.

10 96. The method of claim 94 wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having an additional mutation at codon 153.

15 97. The method of claim 94 wherein the patient-derived segment comprises nucleic acid encoding HIV integrase having an additional mutation at codon 154.

20 98. A method of assessing the effectiveness of protease antiretroviral therapy of an HIV-infected patient comprising:  
(uuuu) collecting a biological sample from the HIV-infected patient;

25 (b) evaluating whether the biological sample contains nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71, 64, 93, 23, 58, and 36; and

30 (c) determining a change in susceptibility to a protease inhibitor.

35 99. The method of claim 98, wherein the mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine(V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

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5 100. The method of claim 99, wherein the protease inhibitor  
is selected from the group consisting of indinavir,  
amprenavir, and saquinavir.

10 101. The method of claim 100, having a mutation at codon 82  
and a secondary mutation at codons selected from the  
group consisting of 84, 48, 23, 73, 53, 33, 74, 20, 90,  
32 and 39 or a mutation at codon 90 and a secondary  
mutation at codons selected from the group consisting  
of 53, 66, 84, 54, 48, 33, 73, 20, 71, 64 and 93,  
15 wherein the protease inhibitor is saquinavir.

102. The method of claim 101, having a mutation at codon 82  
and a secondary mutation at codons selected from the  
group consisting of 84, 48, 23, 73, 53, 33, 74, 20, and  
20 90, or a mutation at codon 90 and a secondary mutation  
at codons selected from the group consisting of 53, 66,  
84, 54, 48, 33, 73, 20, and 71, wherein the change in  
susceptibility in step (c) is a decrease in  
susceptibility to saquinavir.

25 103. The method of claim 101, having a mutation at codon 82  
and a secondary mutation at codons 32 or 39, or a  
mutation at codon 90 and a secondary mutation at codons  
64 or 93, wherein the change in susceptibility in step  
30 (c) is an increase in susceptibility to saquinavir.

104. The method of claim 100, having a mutation at codon 90  
and a secondary mutation at codons selected from the  
group consisting of 53, 95, 54, 84, 82, 46, 13, and 74,  
35 wherein the protease inhibitor is indinavir.

105. The method of claim 104, having a mutation at codon 90  
and a secondary mutation at codons selected from the  
group consisting of 53, 95, 54, 84, 82, and 46, wherein  
40 the change in susceptibility in step (c) is a decrease

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5 in susceptibility to indinavir.

106. The method of claim 104, having a mutation at codon 90 and a secondary mutation at codons 13 or 74, wherein the change in susceptibility in step (c) is an increase in  
10 susceptibility to indinavir.

107. The method of claim 100, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 48, 15 23, 84, 53, 74, 60, 33, 36, 35, 32, and 46 or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 95, 55, 54, 82, 85, 84, 20, 72, 62, 74, 53, 48, 23, 58, 36, 64, 77, and 93.

20 108. The method of claim 107, wherein the protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.

109. The method of claim 108, wherein step (c) is determining  
25 a change in susceptibility to the protease inhibitor greater than 10 fold.

110. The method of claim 108, having a mutation at codon 82 and a secondary mutation at codons selected from the group consisting of 48, 23, 84, 53, 74, 20, 60, 33, 36, 30 35, or a mutation at codon 90 and a secondary mutation at codons selected from the group consisting of 84, 53, 48, 23, 58, 20, 36, and 54, wherein the change in susceptibility in step (c) is a decrease in  
35 susceptibility to saquinavir.

111. The method of claim 108, having a mutation at codon 82 and a secondary mutation at codons 32 or 46, or a mutation at codon 90 and a secondary mutation at codons 40 64, 77, or 93, wherein the change in susceptibility in

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5 step (c) is an increase in susceptibility to saquinavir.

112. The method of claim 108, having a mutation at codon 82  
and a secondary mutation at codons selected from the  
group consisting of 73, 55, 48, 20, 43, 53, and 90, or  
10 a mutation at codon 90 and a secondary mutation at  
codons selected from the group consisting of 95, 55, 54,  
82, 85, 84, 20, 72, and 62, wherein the change in  
susceptibility in step (c) is a decrease in  
susceptibility to indinavir.

15

113. The method of claim 108, having a mutation at codon 82  
and a secondary mutation at codon 13, or a mutation at  
codon 90 and a secondary mutation at codon 74, wherein  
the change in susceptibility in step (c) is an increase  
20 in susceptibility to indinavir.

114. A method of assessing the effectiveness of protease  
antiretroviral therapy of an HIV-infected patient  
comprising:  
25 (a) collecting a biological sample from the  
HIV-infected patient;  
(b) evaluating whether the biological sample contains  
nucleic acid encoding HIV protease having a  
mutation at codon 90 and secondary mutations of at  
30 least three codons; and  
(c) determining a decrease in susceptibility to  
saquinavir.

115. The method of claim 114, wherein in the evaluating step  
35 (b), the nucleic acid encoding HIV protease has  
secondary mutations of at least five codons.

116. The method of claim 114, wherein the secondary mutation  
are selected from the group consisting of codons 10, 20,  
40 52, 53, 54, 66, 71, 73 and 84.

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5 117. A method of assessing the effectiveness of protease  
antiretroviral therapy of an HIV-infected patient  
comprising:

(nnnnn) collecting a biological sample from the  
HIV-infected patient;

10 (b) evaluating whether the biological sample contains  
nucleic acid encoding HIV protease having a  
mutation at codon 82 and secondary mutations at  
codons selected from the group consisting of 33,  
23, 84, 32, 53, 90, 37, 71, 46, 10, 54, 61, 11,  
15 and 46, or a mutation at codon 90 and secondary  
mutations at codons selected from the group  
consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46,  
82, 36, 10, 62, 74, 15, 47, 66, 32, 55, 53, 13,  
and 69; and

20 (c) determining a change in susceptibility to  
amprenavir.

118. The method of claim 117, wherein the mutation at codon  
82 is a substitution of alanine (A), phenylalanine (F),  
25 serine (S), or threonine (T) for valine(V) and the  
mutation at codon 90 is a substitution of methionine (M)  
for leucine (L).

119. The method of claim 118, having a mutation at codon 82  
30 and secondary mutations at codons selected from the  
group consisting of 33, 23, 84, 32, 53, 90, 37, 71, 46,  
10, 54, 11, and 46, or a mutation at codon 90 and  
secondary mutations at codons selected from the group  
consisting of 89, 53, 84, 33, 92, 95, 54, 58, 46, 82,  
35 36, 10, 62, 47, 66, 32, 55, 53, and 13; wherein the  
change in susceptibility in step (c) is a decrease in  
susceptibility to saquinavir.

120. The method of claim 118, having a mutation at codon 82  
40 and a secondary mutation at codon 61, or a mutation at

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5 codon 90 and secondary mutations at codons 74, 15, or 69, wherein the change in susceptibility in step (c) is an increase in susceptibility to saquinavir.

10 121. A resistance test vector comprising an HIV patient-derived segment comprising nucleic acid encoding protease having a mutation at codon 82 and secondary mutations at codons selected from the group consisting of 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and 15 secondary mutations at codons selected from the group consisting of 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71, 64, 93, 23, 58, and 36 and an indicator gene, wherein the expression of the 20 indicator gene is dependent upon the patient-derived segment.

122. The resistance test vector of claim 121, wherein the mutation of the patient derived segment at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) and the mutation at codon 90 is a substitution of methionine (M) for leucine (L).

30 123. A method for determining whether an HIV virus obtained from a patient infected with HIV is resistant to IDV, LPV, NFV and RTV which comprises determining whether a mutation at position 30 from D to N exists in the HIV protease obtained from the patient, wherein the presence 35 of the mutation indicates that the virus is resistant to IDV, LPV, NFV and RTV.

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124. A method for determining whether an HIV virus obtained from a patient infected with HIV is resistant to IDV, LPV, NFV or RTV which comprises determining whether the virus is resistant to any one of IDV, LPV, NFV or RTV, wherein a determination that the virus is resistant to any one of IDV, LPV, NFV or RTV is indicative of the virus being resistant to IDV, LPV, NFV and RTV.

10  
125. A method for determining cross resistance of an HIV virus to RTV and SQV which comprises determining (i) whether position 30 of the HIV protease is D, and (ii) whether the virus is resistant to NFV, wherein a mutation from D to N at position 30 of HIV protease and resistance of the virus to NFV are indicative of cross resistance to IDV and SQV.

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126. A method for determining whether an HIV virus obtained from a patient infected with HIV is resistant to LPV and IND which comprises determining whether position 50 of the HIV protease of the virus is I or V, wherein the determination that position 50 is V is indicative of the virus being resistant to LPV and IND.

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**TABLE A**  
**Summary of Replication Capacity (RC) and**  
**Enzyme Function Results**

	LOW RC (<25% of Ref.*)	MEDIUM RC (26-75% of Ref.)	HIGH RC (>75% of Ref.)
% of Total Tested	41% (55)	45% (59)	14% (19)
PR Processing Defects (%p41>10%)	71% (39)	24% (14)	10% (2)
Impaired RT Activity (<25% of reference)	14% (7)	2% (1)	0%
>10 mutations in Protease	62% (34)	22% (13)	5% (1)
>10X reduced susceptibility to NFV	63% (35)	32% (19)	16% (3)

\*Reference virus: NL4.3